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agcaaacgcg	cctcgacggc	tccaccgatt	gggtcggcct	gtg	aaa	aac	ctc	gac									115
				Val	Lys	Asn	Leu	Asp									5
				1													
atc	gcc	cg	tac	cg	cg	caa	att	atg	ctc	ggc	gaa	atc	ggc	cag	caa	163	
Ile	Ala	Arg	Tyr	Arg	Arg	Gln	Ile	Met	Leu	Gly	Glu	Ile	Gly	Gln	Gln		
				10												20	
aaa	caa	caa	tcg	ctt	ttc	gac	gct	aag	gtc	tcc	gtc	atc	ggc	gca	ggc	211	
Lys	Gln	Gln	Ser	Leu	Phe	Asp	Ala	Lys	Val	Ser	Val	Ile	Gly	Ala	Gly		
			25												35		
ggc	ctc	ggg	tca	ccc	gcc	ctg	ctc	tac	ctt	gct	ggc	gct	ggc	gtc	ggc	259	
Gly	Leu	Gly	Ser	Pro	Ala	Leu	Leu	Tyr	Leu	Ala	Gly	Ala	Gly	Val	Gly		
		40												50			
cac	atc	cac	atc	att	gac	gat	gac	ctc	gtc	gac	ctc	tcc	aac	ctc	cac	307	
His	Ile	His	Ile	Ile	Asp	Asp	Asp	Leu	Val	Asp	Leu	Ser	Asn	Leu	His		
		55												65			
cgc	cag	gtc	att	cac	acc	acc	gct	ggc	gtt	gga	aca	ccc	aag	gcc	gag	355	
Arg	Gln	Val	Ile	His	Thr	Thr	Ala	Gly	Val	Gly	Thr	Pro	Lys	Ala	Glu		
	70												80	85			
tcc	gcg	cg	gaa	gca	atg	ctg	gca	ctg	aac	cct	tcc	gtt	aaa	gtg	acg	403	
Ser	Ala	Arg	Glu	Ala	Met	Leu	Ala	Leu	Asn	Pro	Ser	Val	Lys	Val	Thr		
			90												95	100	
gtt	tct	gtc	agg	cga	ctg	gac	tgg	tca	aat	gca	ctt	tct	gag	ctg	gca	451	
Val	Ser	Val	Arg	Arg	Leu	Asp	Trp	Ser	Asn	Ala	Leu	Ser	Glu	Leu	Ala		
			105												110	115	

gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
 120 125 130

ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc 535
 Leu Ala Ser Trp Ala Ala Lys Leu Gly Ile Pro
 135 140 145

<210> 738

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 738

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
 1 5 10 15

Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
 20 25 30

Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
 35 40 45

Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
 50 55 60

Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
 65 70 75 80

Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
 85 90 95

Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala
 100 105 110

Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn
 115 120 125

Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
 130 135 140

Pro

145

<210> 739

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXN00437

<400> 739

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ccactcattg atcacatcac tggaactctg caaggccacc atg aac act gac ccc 115


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<210> 740
<211> 152
<212> PRT
<213> Corynebacterium glutamicum
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<400> 740
Met Asn Thr Asp Pro Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile
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Asp Ala Phe Leu Thr Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala
20 25 30
Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
35 40 45
Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
50 55 60

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 65 70 75 80
 Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 85 90 95
 Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 100 105 110
 Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 115 120 125
 Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 130 135 140
 Gly Ser Thr Asp Trp Val Gly Leu
 145 150

<210> 741
 <211> 383
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(360)
 <223> FRXA00437

<400> 741
 aaa aac ggc gtc tgc aca gag gcg atg ggc gcg ctg gtc acc ttc gaa 48
 Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 1 5 10 15
 ggc atc gtc cgc gac cac gac ggc ggc gcc cgc gtg acc tcc ctg acc 96
 Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 20 25 30
 tac acc gcg cat ccc acc gcg ccg cag gtc ctt tct gct gtc gcg gac 144
 Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 35 40 45
 tcc atc gtt gaa aaa cac ccg cgc acc cgc ctc tgg acc gcg cac cgc 192
 Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 50 55 60
 acc ggc gcc ttg aaa atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc 240
 Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 65 70 75 80
 tcc gcc cac cgc gcc gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac 288
 Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 85 90 95
 gcc gtc aaa gcc cag gtc ccg atc tgg aaa gag caa acg cgc ctc gac 336
 Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 100 105 110
 ggc tcc acc gat tgg gtc ggc ctg tgaaaaacct cgacatcgcc cgc 383
 Gly Ser Thr Asp Trp Val Gly Leu

115

120

<210> 742

<211> 120

<212> PRT

<213> Corynebacterium glutamicum

<400> 742

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 1 5 10 15

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 20 25 30

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 35 40 45

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 50 55 60

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 65 70 75 80

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 85 90 95

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 100 105 110

Gly Ser Thr Asp Trp Val Gly Leu
 115 120

<210> 743

<211> 591

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(568)

<223> RXN00439

<400> 743

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tcgttaagat ttaccattc aactaacagg agttaattta atg agc gag ctc acc 115
 Met Ser Glu Leu Thr
 1 5

cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163
 His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys
 10 15 20

aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211
 Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg
 25 30 35

ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggc gac 259
 Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp

40	45	50	
gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg			307
Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr			
55	60	65	
ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act			355
Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr			
70	75	80	85
gtg gat ttt ttt gag ctt act gat ggt gtt ccg att gag gct tcg gtg			403
Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg Ile Glu Ala Ser Val			
90	95	100	
aaa acg cgt ggg gtt act ggt gtg gaa atg gag gcg ttg acg gcc gtg			451
Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu Ala Leu Thr Ala Val			
105	110	115	
agc act gcg gcg ctg acg gta tac gac atg atc aag gct gtg gat aag			499
Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile Lys Ala Val Asp Lys			
120	125	130	
atg gcc gtg att gat ggc att cgt gtg ctg tcg aaa act ggc ggt aaa			547
Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser Lys Thr Gly Gly Lys			
135	140	145	
tct ggg gat tgg tct gtt cag tgacagctct gggtatcggt gcg			591
Ser Gly Asp Trp Ser Val Gln			
150	155		

<210> 744

<211> 156

<212> PRT

<213> Corynebacterium glutamicum

<400> 744

Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val			
1	5	10	15
Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly			
20	25	30	
Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly			
35	40	45	
Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met			
50	55	60	
Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro			
65	70	75	80
Leu Gly Lys Ile Thr Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg			
85	90	95	
Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu			
100	105	110	
Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile			
115	120	125	

Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser
 130 135 140

Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val Gln
 145 150 155

<210> 745

<211> 218

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(195)

<223> FRXA00439

<400> 745

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 Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
 1 5 10 15

ggt gtg gaa atg gag gcg ttg acg gcc gtg agc act gcg gcg ctg acg 96
 Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
 20 25 30

gta tac gac atg atc aag gct gtg gat aag atg gcc gtg att gat ggc 144
 Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
 35 40 45

att cgt gtg ctg tcg aaa act ggc ggt aaa tct ggg gat tgg tct gtt 192
 Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
 50 55 60

cag tgacagctct gggtatcggt gcg 218
 Gln
 65

<210> 746

<211> 65

<212> PRT

<213> Corynebacterium glutamicum

<400> 746

Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
 1 5 10 15

Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
 20 25 30

Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
 35 40 45

Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
 50 55 60

Gln
 65

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<220>
<221> CDS
<222> (101) .. (358)
<223> FRXA00442
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<210> 748
<211> 86
<212> PRT
<213> Corynebacterium glutamicum
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<400> 748
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Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly
          20          25          30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly
          35          40          45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met
  50          55          60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro

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65	70	75	80
Leu Gly Lys Ile Thr Val			
	85		
<210> 749			
<211> 582			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(559)			
<223> RXA00440			
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tgctgaaaac tggcggtaaa tctggggatt ggtctgttca gtg aca gct ctg gtt 115			
Val Thr Ala Leu Val 1 5			
atc gtt gcg tcc act cgc gcc gct gcc ggg gtg tat gag gat cgc tct 163			
Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val Tyr Glu Asp Arg Ser 10 15 20			
ggc cca att ttg gtg tcg tgg ctg cgt gca aaa ggt ttt gac aca ccc 211			
Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys Gly Phe Asp Thr Pro 25 30 35			
gcc ccc gtg atc gtg gcg gac gcc aac ctg ccc gca ttc ctg gac gag 259			
Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro Ala Phe Leu Asp Glu 40 45 50			
ctg gaa ttt ccg cag gta gta ctt att tca ggc ggc acc gga ctc acg 307			
Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly Gly Thr Gly Leu Thr 55 60 65			
cct gat gac atc acc gtg gac act tta atc ccg cgc ctc gac aaa gaa 355			
Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro Arg Leu Asp Lys Glu 70 75 80 85			
atc ccc ggc atc gcc cac gct ttt tgg aat tac agc atg gac gcc gtc 403			
Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr Ser Met Asp Ala Val 90 95 100			
ccg acc gca gta ttg tcg cgc acc gtc gcg ggc acc atc ggc ggc agt 451			
Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly Thr Ile Gly Gly Ser 105 110 115			
ttc atc atg gcg ctg ccc ggc tcc acg ggt gcg gcg cgc gat gcc acc 499			
Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala Ala Arg Asp Ala Thr 120 125 130			
gct gtc ctc gac cca ctc att gat cac atc act gga act ctg caa ggc 547			
Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr Gly Thr Leu Gln Gly 135 140 145			
cac cat gaa cac tgaccccgct tacgtcgccg aac 582			
His His Glu His			

150

<210> 750

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 750

Val Thr Ala Leu Val Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val
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Tyr Glu Asp Arg Ser Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys
 20 25 30

Gly Phe Asp Thr Pro Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro
 35 40 45

Ala Phe Leu Asp Glu Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly
 50 55 60

Gly Thr Gly Leu Thr Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro
 65 70 75 80

Arg Leu Asp Lys Glu Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr
 85 90 95

Ser Met Asp Ala Val Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly
 100 105 110

Thr Ile Gly Gly Ser Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala
 115 120 125

Ala Arg Asp Ala Thr Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr
 130 135 140

Gly Thr Leu Gln Gly His His Glu His
 145 150

<210> 751

<211> 1287

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1264)

<223> RXN00441

<400> 751

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agcgttacga ttgttttcca aggtgagaaa ggtttaattg atg tct cgt tcg ccg 115
 Met Ser Arg Ser Pro
 1 5

gag caa cat ttg gca gaa att tca gcg ctg ctt ccc cca caa aag tcc 163
 Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu Pro Pro Gln Lys Ser
 10 15 20

acg	ttc	gtg	aat	ctg	cgc	gaa	gcg	ttg	gga	cgc	cgc	acg	ttt	tca	gcg	211
Thr	Phe	Val	Asn	Leu	Arg	Glu	Ala	Leu	Gly	Arg	Arg	Thr	Phe	Ser	Ala	
			25					30					35			
gtc	act	gcg	cag	tgg	gat	tcg	cca	cgt	ttt	gat	aat	tcc	caa	atg	gat	259
Val	Thr	Ala	Gln	Trp	Asp	Ser	Pro	Arg	Phe	Asp	Asn	Ser	Gln	Met	Asp	
		40					45					50				
ggc	ttc	gcg	ctt	ggc	ccc	tca	cat	ctt	aac	ggg	ggc	acc	ttc	gca	gtc	307
Gly	Phe	Ala	Leu	Gly	Pro	Ser	His	Leu	Asn	Gly	Gly	Thr	Phe	Ala	Val	
	55					60					65					
ggg	cca	acc	att	ccc	gct	ggg	cat	gat	cct	gat	cag	tgg	tac	cca	cga	355
Gly	Pro	Thr	Ile	Pro	Ala	Gly	His	Asp	Pro	Asp	Gln	Trp	Tyr	Pro	Arg	
	70				75				80						85	
ggc	atc	gaa	aaa	gac	atc	gcg	ccg	att	atg	acg	ggg	gcg	cgc	ctt	cct	403
Gly	Ile	Glu	Lys	Asp	Ile	Ala	Pro	Ile	Met	Thr	Gly	Ala	Arg	Leu	Pro	
				90					95					100		
aaa	aac	acc	gcc	gcg	atc	att	cct	gtg	gag	aaa	acc	aca	ccg	gga	aat	451
Lys	Asn	Thr	Ala	Ala	Ile	Ile	Pro	Val	Glu	Lys	Thr	Thr	Pro	Gly	Asn	
			105				110						115			
ttc	gac	gcc	cca	cag	gta	gaa	atc	ccc	gcc	acc	ccg	caa	ggg	cag	ttc	499
Phe	Asp	Ala	Pro	Gln	Val	Glu	Ile	Pro	Ala	Thr	Pro	Gln	Gly	Gln	Phe	
		120					125					130				
ata	cgg	ttg	cag	ggg	tcg	gat	att	act	gcc	ggc	gac	gag	atc	att	cca	547
Ile	Arg	Leu	Gln	Gly	Ser	Asp	Ile	Thr	Ala	Gly	Asp	Glu	Ile	Ile	Pro	
	135					140					145					
gca	ggg	acg	gag	ctt	aac	tcg	gtg	cac	atc	ggg	gtg	ttg	gct	agt	cag	595
Ala	Gly	Thr	Glu	Leu	Asn	Ser	Val	His	Ile	Gly	Val	Leu	Ala	Ser	Gln	
	150				155					160					165	
tcg	atc	aag	agc	att	gaa	gtc	gca	gca	aag	cca	cgt	gtc	ctc	atc	atc	643
Ser	Ile	Lys	Ser	Ile	Glu	Val	Ala	Ala	Lys	Pro	Arg	Val	Leu	Ile	Ile	
			170						175					180		
acc	ggc	ggg	tct	gaa	att	tca	gaa	cag	cac	gga	ccc	gcc	acg	atc	cct	691
Thr	Gly	Gly	Ser	Glu	Ile	Ser	Glu	Gln	His	Gly	Pro	Ala	Thr	Ile	Pro	
			185					190					195			
gat	gcc	aac	ggc	cct	ctg	ctt	cgt	tcc	ctg	tgc	gcc	cgc	aac	aat	atc	739
Asp	Ala	Asn	Gly	Pro	Leu	Leu	Arg	Ser	Leu	Cys	Ala	Arg	Asn	Asn	Ile	
		200					205					210				
gag	gtc	atc	gcg	gga	ctg	cac	acc	aac	gac	gat	cct	gaa	cga	ctc	cgc	787
Glu	Val	Ile	Ala	Gly	Leu	His	Thr	Asn	Asp	Asp	Pro	Glu	Arg	Leu	Arg	
	215					220					225					
ttt	gaa	ctg	gaa	aac	gcc	att	gac	cag	tat	caa	ccg	gat	gtc	atc	atc	835
Phe	Glu	Leu	Glu	Asn	Ala	Ile	Asp	Gln	Tyr	Gln	Pro	Asp	Val	Ile	Ile	
	230				235					240					245	
acc	tct	ggc	ggg	atc	agc	cac	ggg	aaa	ttt	gag	gtg	ttt	agg	cag	atc	883
Thr	Ser	Gly	Gly	Ile	Ser	His	Gly	Lys	Phe	Glu	Val	Phe	Arg	Gln	Ile	
				250				255						260		
ctc	gaa	ggc	acc	ccg	aac	tcc	tgg	ttt	gga	cat	gtc	gat	cag	cag	cct	931

Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His Val Asp Gln Gln Pro
 265 270 275
 ggc ggt cct caa ggc atc tcc act ttt gct gaa act cct gtc att tca 979
 Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu Thr Pro Val Ile Ser
 280 285 290
 ctt ccc gga aat ccg att tcc acc ttg gtg agt ttc aca ctt ttg gtc 1027
 Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser Phe Thr Leu Leu Val
 295 300 305
 gcg cca gcg ctc aac cgc cag ccg ctc cgc cac ctc gat gcc cgc atc 1075
 Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His Leu Asp Ala Arg Ile
 310 315 320 325
 acc gct ccg gtc cag ggc ttg caa gac aat cgc gag caa ttc ctt cgc 1123
 Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg Glu Gln Phe Leu Arg
 330 335 340
 ggc acc atc agt tac cgc aac ggg cca cgt cct cgc cac gcc tct cct 1171
 Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro Arg His Ala Ser Pro
 345 350 355
 ggg cac cag ttc cca cct gct ggt tca agc tgc cac cgc aga ctg tct 1219
 Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys His Arg Arg Leu Ser
 360 365 370
 gat cag gat ccc ggc gcg gac tac ggt gga gga aaa cga cat cgt 1264
 Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly Lys Arg His Arg
 375 380 385
 taagatttac ccattcaact aac 1287

<210> 752

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 752

Met Ser Arg Ser Pro Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu
 1 5 10 15
 Pro Pro Gln Lys Ser Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg
 20 25 30
 Arg Thr Phe Ser Ala Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp
 35 40 45
 Asn Ser Gln Met Asp Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly
 50 55 60
 Gly Thr Phe Ala Val Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp
 65 70 75 80
 Gln Trp Tyr Pro Arg Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr
 85 90 95
 Gly Ala Arg Leu Pro Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys
 100 105 110

Thr Thr Pro Gly Asn Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr
 115 120 125
 Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly
 130 135 140
 Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly
 145 150 155 160
 Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro
 165 170 175
 Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly
 180 185 190
 Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys
 195 200 205
 Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp
 210 215 220
 Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln
 225 230 235 240
 Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu
 245 250 255
 Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His
 260 265 270
 Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu
 275 280 285
 Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser
 290 295 300
 Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His
 305 310 315 320
 Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg
 325 330 335
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<213> *Corynebacterium glutamicum*

<220>

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<222> (1)..(792)

<223> FRXA00441

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Val	His	Ile	Gly	Val	Leu	Ala	Ser	Gln	Ser	Ile	Lys	Ser	Ile	Glu	Val	
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Pro	Leu	Arg	His	Leu	Asp	Ala	Arg	Ile	Thr	Ala	Pro	Val	Gln	Gly	Leu	
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 Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp
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<210> 754

<211> 264

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 754

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Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val
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Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser
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Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu
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Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His
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Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile
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Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His
 115 120 125

Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser
 130 135 140

Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser
 145 150 155 160

Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser
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Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln
 180 185 190

Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu
 195 200 205

Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn
 210 215 220

Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala
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Tyr Gly Gly Gly Lys Arg His Arg
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<213> Corynebacterium glutamicum

<220>

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<222> (101)..(2335)

<223> RXN02085

<400> 755

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Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
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His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser	
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Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg	
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Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg	
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 Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp
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gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc 2083
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 Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val
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 Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly
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 Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
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<212> PRT

<213> Corynebacterium glutamicum

<400> 756

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Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
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Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
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Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
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Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
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Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu

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 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
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 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
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 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
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 Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
 645 650 655
 Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
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 Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
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<220>

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<222> (101)..(1900)

<223> FRXA02085

<400> 757

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Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
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Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
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		200					205					210					
gat	gtt	gct	cct	gag	gtt	ttg	gag	cag	gtc	cgc	gct	ggg	tac	acc	act	787	
Asp	Val	Ala	Pro	Glu	Val	Leu	Glu	Gln	Val	Arg	Ala	Gly	Tyr	Thr	Thr		
		215					220					225					
ttg	gct	aag	cgc	gat	ggc	gtg	ttt	gtc	aat	act	tac	ttc	ggc	tct	ggc	835	
Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr	Tyr	Phe	Gly	Ser	Gly		
230					235					240				245			
gat	cag	gcg	ctg	aac	act	ctt	gcg	ggc	atc	ggc	ctt	ggc	gcg	att	ggc	883	
Asp	Gln	Ala	Leu	Asn	Thr	Leu	Ala	Gly	Ile	Gly	Leu	Gly	Ala	Ile	Gly		
				250					255					260			
gtt	gac	ttg	gtc	acc	cat	ggc	gtc	act	gag	ctt	gct	gcg	tgg	aag	ggg	931	
Val	Asp	Leu	Val	Thr	His	Gly	Val	Thr	Glu	Leu	Ala	Ala	Trp	Lys	Gly		
				265					270					275			
gag	gag	ctg	ctg	gtt	gcg	ggc	atc	gtt	gat	ggg	cgt	aac	att	tgg	cgc	979	
Glu	Glu	Leu	Leu	Val	Ala	Gly	Ile	Val	Asp	Gly	Arg	Asn	Ile	Trp	Arg		
		280					285					290					
acc	gac	ctg	tgt	gct	gct	ctt	gct	tcc	ctg	aag	cgc	ctg	gca	gct	cgc	1027	
Thr	Asp	Leu	Cys	Ala	Ala	Leu	Ala	Ser	Leu	Lys	Arg	Leu	Ala	Ala	Arg		
		295					300					305					
ggc	cca	atc	gca	gtg	tct	acc	tct	tgt	tca	ctg	ctg	cac	gtt	cct	tac	1075	
Gly	Pro	Ile	Ala	Val	Ser	Thr	Ser	Cys	Ser	Leu	Leu	His	Val	Pro	Tyr		
310					315					320					325		
acc	ctc	gag	gct	gag	aac	att	gag	cct	gag	gtc	cgc	gac	tgg	ctt	gcc	1123	
Thr	Leu	Glu	Ala	Glu	Asn	Ile	Glu	Pro	Glu	Val	Arg	Asp	Trp	Leu	Ala		
				330					335					340			
ttc	ggc	tcg	gag	aag	atc	acc	gag	gtc	aag	ctg	ctt	gcc	gac	gcc	cta	1171	
Phe	Gly	Ser	Glu	Lys	Ile	Thr	Glu	Val	Lys	Leu	Leu	Ala	Asp	Ala	Leu		
				345					350					355			
gcc	ggc	aac	atc	gac	gcg	gct	gcg	ttc	gat	gcg	gcg	tcc	gca	gca	att	1219	
Ala	Gly	Asn	Ile	Asp	Ala	Ala	Ala	Phe	Asp	Ala	Ala	Ser	Ala	Ala	Ile		
		360					365					370					
gct	tct	cga	cgc	acc	tcc	cca	cgc	acc	gca	cca	atc	acg	cag	gaa	ctc	1267	
Ala	Ser	Arg	Arg	Thr	Ser	Pro	Arg	Thr	Ala	Pro	Ile	Thr	Gln	Glu	Leu		
		375					380					385					
cct	ggc	cgt	agc	cgt	gga	tcc	ttc	gac	act	cgt	gtt	acg	ctg	cag	gag	1315	
Pro	Gly	Arg	Ser	Arg	Gly	Ser	Phe	Asp	Thr	Arg	Val	Thr	Leu	Gln	Glu		
390					395					400					405		
aag	tca	ctg	gag	ctt	cca	gct	ctg	cca	acc	acc	acc	att	ggg	tct	ttc	1363	
Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe		
				410					415					420			
cca	cag	acc	cca	tcc	att	cgt	tct	gct	cgc	gct	cgt	ctg	cgc	aag	gaa	1411	
Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala	Arg	Leu	Arg	Lys	Glu		
				425					430					435			

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tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat 1459
Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
      440                      445                      450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac 1507
Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
      455                      460                      465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc 1555
Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
470                      475                      480                      485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc 1603
Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
      490                      495                      500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg 1651
Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
      505                      510                      515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag 1699
Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
      520                      525                      530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc 1747
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
      535                      540                      545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca 1795
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
550                      555                      560                      565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag 1843
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
      570                      575                      580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg 1891
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
      585                      590                      595

aga cgt cga taagcctgcc tacctgcagt ggt 1923
Arg Arg
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<210> 758

<211> 600

<212> PRT

<213> Corynebacterium glutamicum

<400> 758

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Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
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Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
      20                      25                      30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
      35                      40                      45

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Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro

370					375					380				
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg														
385					390				395					400
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr														
			405					410					415	
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala														
			420					425					430	
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met														
			435					440					445	
Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu														
			450					455					460	
Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr														
			465					470					475	480
Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val														
			485					490					495	
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn														
			500					505					510	
Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln														
			515					520					525	
Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr														
			530					535					540	
Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr														
			545					550					555	560
Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile														
			565					570					575	
Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu														
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Leu Leu Pro Ala Thr Arg Arg Arg														
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<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (580)

<223> FRXA02086

<400> 759

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aacgatctca tcgaggctgg cgcgaagatc atccaggtgg atg agc ctg cga ttc 115

Met Ser Leu Arg Phe

1

5


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gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
      10      15      20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
      25      30      35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
      40      45      50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
      55      60      65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
      70      75      80      85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
      90      95      100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
      105      110      115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
      120      125      130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
      135      140      145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
150      155      160

aac 603

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<210> 760

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 760

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Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
      20      25      30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
      35      40      45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
      50      55      60

```

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
 115 120 125
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
 130 135 140
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
 145 150 155 160

<210> 761
 <211> 1326
 <212> DNA
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<220>
 <221> CDS
 <222> (101)..(1303)
 <223> RXN02648

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 Met Ser Gln Asn Arg 5
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu 20
 10 15
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe 35
 25 30
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val 50
 40 45 50
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr 65
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg 85
 70 75 80
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403

Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg	Trp	Ala	Ser	Gln	Glu		
				90					95					100			
gca	gtg	cgt	tcc	acc	cct	ggc	aac	atc	gag	ctg	acc	agc	ttc	tct	gat	451	
Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu	Thr	Ser	Phe	Ser	Asp		
			105					110					115				
cgt	cgc	gac	cgc	gca	ttg	ttc	agc	gaa	gca	tac	gag	gat	cca	gta	tct	499	
Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr	Glu	Asp	Pro	Val	Ser		
			120					125					130				
ggc	atc	ttc	acc	ggc	cgc	gct	tct	gtg	ggc	aac	cca	gag	ttc	acc	gga	547	
Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn	Pro	Glu	Phe	Thr	Gly		
	135					140					145						
cct	att	acc	tac	att	ggc	cag	gaa	gaa	act	cag	acg	gat	gtt	gat	ctg	595	
Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Val	Asp	Leu		
	150				155					160					165		
ctg	aag	aag	ggc	atg	aac	gca	gcg	gga	gct	acc	gac	ggc	ttc	gtt	gca	643	
Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala		
				170					175					180			
gca	cta	tcc	cca	gga	tct	gca	gct	cga	ttg	acc	aac	aag	ttc	tac	gac	691	
Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp		
			185					190					195				
act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gcg	ctt	tcc	cag	gaa	739	
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu		
		200					205					210					
tac	aag	atc	atc	acc	gat	gca	ggt	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787	
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro		
	215					220					225						
gac	ttg	gca	gaa	gca	tgg	gat	cag	atc	aac	cca	gag	cca	agc	gtg	aag	835	
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys		
	230				235					240					245		
gat	tac	ttg	gac	tgg	atc	ggt	aca	cgc	atc	gat	gcc	atc	aac	agt	gca	883	
Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp	Ala	Ile	Asn	Ser	Ala		
			250						255					260			
gtg	aag	ggc	ctt	cca	aag	gaa	cag	acc	cgc	ctg	cac	atc	tgc	tgg	ggc	931	
Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile	Cys	Trp	Gly		
			265					270					275				
tct	tgg	cac	gga	cca	cac	gtc	act	gac	atc	cca	ttc	ggc	gac	atc	att	979	
Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly	Asp	Ile	Ile		
		280					285					290					
ggc	gag	atc	ctg	cgc	gca	gag	gtc	ggt	ggc	ttc	tcc	ttc	gaa	ggc	gca	1027	
Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe	Glu	Gly	Ala		
	295					300					305						
tct	cct	cgt	cac	gca	cac	gag	tgg	cgt	gta	tgg	gaa	gaa	aac	aag	ctt	1075	
Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu	Asn	Lys	Leu		
	310				315				320						325		
cct	gaa	ggc	tct	gtt	atc	tac	cct	ggt	gtt	gtg	tct	cac	tcc	atc	aac	1123	
Pro	Glu	Gly	Ser	Val	Ile	Tyr	Pro	Gly	Val	Val	Ser	His	Ser	Ile	Asn		

330										335					340					
gct	gtg	gag	cac	cca	cgc	ctg	gtt	gct	gat	cgt	atc	gtt	cag	ttc	gcc	1171				
Ala	Val	Glu	His	Pro	Arg	Leu	Val	Ala	Asp	Arg	Ile	Val	Gln	Phe	Ala					
345					350					355										
aag	ctt	gtt	ggc	cct	gag	aac	gtc	att	gcg	tcc	act	gac	tgt	ggt	ctg	1219				
Lys	Leu	Val	Gly	Pro	Glu	Asn	Val	Ile	Ala	Ser	Thr	Asp	Cys	Gly	Leu					
360					365					370										
ggc	gga	cgt	ctg	cat	tcc	cag	atc	gca	tggt	gca	aag	ctg	gag	tcc	cta	1267				
Gly	Gly	Arg	Leu	His	Ser	Gln	Ile	Ala	Trp	Ala	Lys	Leu	Glu	Ser	Leu					
375					380					385										
gta	gag	ggc	gct	cgc	att	gca	tca	aag	gaa	ctg	ttc	taagctagac				1313				
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<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 762

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Thr	Pro	Glu	Leu	Leu	Asp	Ala	Asn	Ile	Lys	Arg	Ser	Asn	Gly	Glu	Ile
		20					25						30		

Gly	Glu	Glu	Glu	Phe	Phe	Gln	Ile	Leu	Gln	Ser	Ser	Val	Asp	Asp	Val
		35					40					45			

Ile	Lys	Arg	Gln	Val	Asp	Leu	Gly	Ile	Asp	Ile	Leu	Asn	Glu	Gly	Glu
	50					55					60				

Tyr	Gly	His	Val	Thr	Ser	Gly	Ala	Val	Asp	Phe	Gly	Ala	Trp	Trp	Asn
65					70				75						80

Tyr	Ser	Phe	Thr	Arg	Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg
				85					90					95	

Trp	Ala	Ser	Gln	Glu	Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu
			100					105					110		

Thr	Ser	Phe	Ser	Asp	Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr
		115					120					125			

Glu	Asp	Pro	Val	Ser	Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn
	130					135					140				

Pro	Glu	Phe	Thr	Gly	Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln
145					150					155					160

Thr	Asp	Val	Asp	Leu	Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr
				165					170					175	

Asp	Gly	Phe	Val	Ala	Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

180					185					190					
Asn	Lys	Phe	Tyr	Asp	Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp
		195					200					205			
Ala	Leu	Ser	Gln	Glu	Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val
	210					215					220				
Gln	Leu	Asp	Ala	Pro	Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro
225					230					235					240
Glu	Pro	Ser	Val	Lys	Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp
				245					250					255	
Ala	Ile	Asn	Ser	Ala	Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu
			260					265					270		
His	Ile	Cys	Trp	Gly	Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro
		275					280					285			
Phe	Gly	Asp	Ile	Ile	Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe
	290					295					300				
Ser	Phe	Glu	Gly	Ala	Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp
305					310					315					320
Glu	Glu	Asn	Lys	Leu	Pro	Glu	Gly	Ser	Val	Ile	Tyr	Pro	Gly	Val	Val
			325						330					335	
Ser	His	Ser	Ile	Asn	Ala	Val	Glu	His	Pro	Arg	Leu	Val	Ala	Asp	Arg
			340					345					350		
Ile	Val	Gln	Phe	Ala	Lys	Leu	Val	Gly	Pro	Glu	Asn	Val	Ile	Ala	Ser
	355					360					365				
Thr	Asp	Cys	Gly	Leu	Gly	Gly	Arg	Leu	His	Ser	Gln	Ile	Ala	Trp	Ala
	370					375					380				
Lys	Leu	Glu	Ser	Leu	Val	Glu	Gly	Ala	Arg	Ile	Ala	Ser	Lys	Glu	Leu
385				390						395					400
Phe															

<210> 763

<211> 548

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(525)

<223> FRXA02648

<400> 763

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Asp	Ala	Pro	Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	
1				5				10						15		

agc	gtg	aag	gat	tac	ttg	gac	tgg	atc	ggc	aca	cgc	atc	gat	gcc	atc	96
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Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
      20                      25                      30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
      35                      40                      45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
      50                      55                      60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
      65                      70                      75                      80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
      85                      90                      95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
      100                      105                      110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
      115                      120                      125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
      130                      135                      140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
      145                      150                      155                      160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
      165                      170                      175

taagctagac aacgagggtt gct 548

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<210> 764

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 764

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1                      5                      10                      15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
      20                      25                      30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
      35                      40                      45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
      50                      55                      60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe

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65		70		75		80
Glu Gly Ala Ser	Pro Arg His Ala His	Glu Trp Arg Val Trp	Glu Glu			
	85	90	95			
Asn Lys Leu	Pro Glu Gly Ser Val	Ile Tyr Pro Gly Val	Val Ser His			
	100	105	110			
Ser Ile Asn Ala	Val Glu His Pro Arg	Leu Val Ala Asp	Arg Ile Val			
	115	120	125			
Gln Phe Ala Lys	Leu Val Gly Pro Glu	Asn Val Ile Ala	Ser Thr Asp			
	130	135	140			
Cys Gly Leu Gly	Gly Arg Leu His Ser	Gln Ile Ala Trp	Ala Lys Leu			
145	150	155	160			
Glu Ser Leu Val	Glu Gly Ala Arg	Ile Ala Ser Lys	Glu Leu Phe			
	165	170	175			

<210> 765

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658

<400> 765

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gagtttgata ctttctttcg acttttagat tggattttca	atg agc cag aac cgc	115
	Met Ser Gln Asn Arg	
	1 5	

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt	163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu	
10 15 20	

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc	211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe	
25 30 35	

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt	259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val	
40 45 50	

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc	307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr	
55 60 65	

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc	355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg	
70 75 80 85	

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa	403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu	
90 95 100	

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 766

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 766

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala
 225

<210> 767
 <211> 513
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(490)
 <223> RXA01516

<400> 767
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 gttgatgttg ccgcattgtg gcgaagtgga ggaactcacc atg gct gat cgt att 115
 Met Ala Asp Arg Ile
 1 5
 gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt 163
 Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe
 10 15 20
 gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg 211
 Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met
 25 30 35
 gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259
 Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp
 40 45 50
 tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc 307
 Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser
 55 60 65
 agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg 355
 Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met
 70 75 80 85

gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc 403
 Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro
 90 95 100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga 451
 Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg
 105 110 115

cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc 500
 Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala
 120 125 130

agttttgtcc atc 513

<210> 768

<211> 130

<212> PRT

<213> Corynebacterium glutamicum

<400> 768

Met Ala Asp Arg Ile Glu Leu Lys Gly Leu Glu Cys Phe Gly His His
 1 5 10 15

Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp
 20 25 30

Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu
 35 40 45

Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile
 50 55 60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser
 65 70 75 80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val
 85 90 95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser
 115 120 125

Asn Ala
 130

<210> 769

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> RXA01515

<400> 769

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ctcccgcgct gaggtgttct ccctgattcg ggggcactaa atg aac gta tcc tct 115
                                         Met Asn Val Ser Ser
                                         1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163
Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr
                        10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211
Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala
                        25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259
Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
                        40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307
Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
                        55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
                        70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403
Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
                        90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451
Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu
                        105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499
Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
                        120 125 130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547
Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
                        135 140 145

gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
                        150 155 160 165

gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
                        170 175 180

gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
                        185 190 195

cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
                        200 205 210

ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787
Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
                        215 220 225

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cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
 230 235 240 245

gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
 250 255 260

gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
 265 270 275

agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975
 Ser Gly Gly Thr His His Gly
 280

<210> 770

<211> 284

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 770

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly
 1 5 10 15

Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile
 20 25 30

Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45

Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60

Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80

Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala
 85 90 95

Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp
 100 105 110

Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu
 115 120 125

Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly
 130 135 140

Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val
 145 150 155 160

His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val
 165 170 175

Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser
 180 185 190

Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser

195	200	205
Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala		
210	215	220
Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp		
225	230	235 240
Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp		
	245	250 255
Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val		
	260	265 270
Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly		
275	280	

<210> 771

<211> 859

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA02024

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Met Ser Ser Leu Pro	
1 5	

gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag	163
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys	
10 15 20	

ggc ggc aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val	
25 30 35	

att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly	
40 45 50	

ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro	
55 60 65	

atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val	
70 75 80 85	

gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala	
90 95 100	

acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln	

105					110					115						
gta	gca	ggg	cag	cac	aag	gtg	ggt	tat	gtc	tgc	tcg	cac	acc	ggc	ggg	499
Val	Ala	Gly	Gln	His	Lys	Val	Gly	Tyr	Val	Cys	Ser	His	Thr	Gly	Gly	
		120						125					130			
gtg	att	cca	aga	acg	cga	cca	tat	cgg	gtg	cat	ttc	gat	gac	atc	gtg	547
Val	Ile	Pro	Arg	Thr	Arg	Pro	Tyr	Arg	Val	His	Phe	Asp	Asp	Ile	Val	
		135						140					145			
gcc	gat	gta	att	acg	gag	acc	acc	aaa	ttg	gca	gag	caa	gct	gtt	cgt	595
Ala	Asp	Val	Ile	Thr	Glu	Thr	Thr	Lys	Leu	Ala	Glu	Gln	Ala	Val	Arg	
		150				155					160				165	
gcc	ggg	gtg	cca	gag	gaa	cgg	gtg	ttt	att	gat	ccc	acc	cat	gat	ttc	643
Ala	Gly	Val	Pro	Glu	Glu	Arg	Val	Phe	Ile	Asp	Pro	Thr	His	Asp	Phe	
				170						175					180	
ggg	aaa	aac	acc	ttc	cac	gga	ctg	gag	ctt	tta	cga	cgg	atc	gat	gag	691
Gly	Lys	Asn	Thr	Phe	His	Gly	Leu	Glu	Leu	Leu	Arg	Arg	Ile	Asp	Glu	
			185						190						195	
gtg	gtt	gcc	acg	ggc	tgg	ccg	gtg	ctg	atg	gcc	ttg	agt	aat	aag	gat	739
Val	Val	Ala	Thr	Gly	Trp	Pro	Val	Leu	Met	Ala	Leu	Ser	Asn	Lys	Asp	
		200						205					210			
ttc	att	ggg	gaa	act	ttg	gaa	agg	ggc	gtc	gat	aag	cgt	gtt	gct	ggc	787
Phe	Ile	Gly	Glu	Thr	Leu	Glu	Arg	Gly	Val	Asp	Lys	Arg	Val	Ala	Gly	
		215					220					225				
acg	ctt	gct	gcc	act	gcc	tgg	gcg	gcg	gcg	cgc	ggc	gtt	gcg	gct	ttt	835
Thr	Leu	Ala	Ala	Thr	Ala	Trp	Ala	Ala	Ala	Arg	Gly	Val	Ala	Ala	Phe	
		230				235				240					245	
cgc	gtg	cat	gaa	gtt	gcg	gaa	acc									859
Arg	Val	His	Glu	Val	Ala	Glu	Thr									
				250												

<210> 772

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 772

Met	Ser	Ser	Leu	Pro	Val	Ile	Met	Ala	Ile	Val	Asn	Arg	Thr	Pro	Asp	
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Ser	Phe	Tyr	Asp	Lys	Gly	Ala	Thr	Phe	Glu	Asp	Thr	Ala	Ala	Leu	Asn	
			20					25					30			
Arg	Ala	Ala	Glu	Val	Ile	Glu	Gln	Gly	Ala	Gly	Ile	Val	Asp	Ile	Gly	
			35				40						45			
Gly	Val	Lys	Ala	Gly	Pro	Gly	Asp	Phe	Val	Ser	Ala	Glu	Glu	Glu	Ile	
		50				55					60					
Asp	Arg	Val	Val	Pro	Ile	Ile	Ala	Ala	Val	Arg	Glu	Arg	Phe	Pro	Asp	
		65			70					75					80	
Ile	Asp	Ile	Ser	Val	Asp	Thr	Trp	Arg	Ala	Ser	Val	Ala	Asp	Val	Ala	

85										90					95				
Val	Ala	His	Gly	Ala	Thr	Leu	Ile	Asn	Asp	Thr	Trp	Ala	Gly	His	Asp				
			100					105					110						
His	Glu	Leu	Val	Gln	Val	Ala	Gly	Gln	His	Lys	Val	Gly	Tyr	Val	Cys				
		115					120					125							
Ser	His	Thr	Gly	Gly	Val	Ile	Pro	Arg	Thr	Arg	Pro	Tyr	Arg	Val	His				
	130					135					140								
Phe	Asp	Asp	Ile	Val	Ala	Asp	Val	Ile	Thr	Glu	Thr	Thr	Lys	Leu	Ala				
145					150					155					160				
Glu	Gln	Ala	Val	Arg	Ala	Gly	Val	Pro	Glu	Glu	Arg	Val	Phe	Ile	Asp				
			165					170						175					
Pro	Thr	His	Asp	Phe	Gly	Lys	Asn	Thr	Phe	His	Gly	Leu	Glu	Leu	Leu				
		180						185					190						
Arg	Arg	Ile	Asp	Glu	Val	Val	Ala	Thr	Gly	Trp	Pro	Val	Leu	Met	Ala				
		195					200					205							
Leu	Ser	Asn	Lys	Asp	Phe	Ile	Gly	Glu	Thr	Leu	Glu	Arg	Gly	Val	Asp				
	210					215					220								
Lys	Arg	Val	Ala	Gly	Thr	Leu	Ala	Ala	Thr	Ala	Trp	Ala	Ala	Ala	Arg				
225					230					235					240				
Gly	Val	Ala	Ala	Phe	Arg	Val	His	Glu	Val	Ala	Glu	Thr							
			245					250											

<210> 773

<211> 684

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(661)

<223> RXA01719

<400> 773

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cgaggacggt	ctggttgatg	ttgtgctggg	gagaatgtaa	atg	aat	atc	atc	att	115
				Met	Asn	Ile	Ile	Ile	
				1				5	

ctt	gct	ggt	ggc	gag	ggt	aaa	cgc	atg	ggt	ggg	gtg	gat	aag	gct	gct	163
Leu	Ala	Gly	Gly	Glu	Gly	Lys	Arg	Met	Gly	Gly	Val	Asp	Lys	Ala	Ala	
				10					15					20		

gtg	gcg	gtg	gat	ggt	cgc	acg	ctg	ctg	gat	atc	ctg	ctt	tca	cag	ctg	211
Val	Ala	Val	Asp	Gly	Arg	Thr	Leu	Leu	Asp	Ile	Leu	Leu	Ser	Gln	Leu	
			25					30					35			

gat	cca	gaa	gat	gac	gtc	gtg	gtg	gtt	tcc	ccc	gcg	atc	atc	gac	gga	259
Asp	Pro	Glu	Asp	Asp	Val	Val	Val	Val	Ser	Pro	Ala	Ile	Ile	Asp	Gly	
		40					45					50				

atc acg act gtc tgc gag gaa cct ccg ctt ggc ggg ccg gtc gcg gga 307
 Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly Gly Pro Val Ala Gly
 55 60 65

atc gag gca ggg ctg aat tct ttt gag cac gcc cat gaa ttc act gcg 355
 Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala His Glu Phe Thr Ala
 70 75 80 85

att ctt gcc gtg gac gcg cct tat tct gca gcg atg ctg ccc cta ctt 403
 Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala Met Leu Pro Leu Leu
 90 95 100

cag gca cag att ggc aaa gcc gat gtg gcc gta acc ctt gct gcc gat 451
 Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val Thr Leu Ala Ala Asp
 105 110 115

ggc tgg gta caa ccg ttg tgc gcg ctg tgg aga agt ggc agc cta gaa 499
 Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg Ser Gly Ser Leu Glu
 120 125 130

gcg gtg att cac agc ctg ggc gag act aga aat cga ccg gca aaa gcg 547
 Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn Arg Pro Ala Lys Ala
 135 140 145

tta ctg aag caa gcg gga cac att gtg gaa gtg ggt ggc gat ggc act 595
 Leu Leu Lys Gln Ala Gly His Ile Val Glu Val Gly Gly Asp Gly Thr
 150 155 160 165

gaa aaa gac tac gat acg gtg gct gaa ctg gag gta ttg ggc aac gta 643
 Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu Val Leu Gly Asn Val
 170 175 180

acg ctc cct aaa gcc cac tgatgagaaa cgtgagctct gct 684
 Thr Leu Pro Lys Ala His
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<210> 774

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 774

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Val Asp Lys Ala Ala Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile
 20 25 30

Leu Leu Ser Gln Leu Asp Pro Glu Asp Asp Val Val Val Val Ser Pro
 35 40 45

Ala Ile Ile Asp Gly Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly
 50 55 60

Gly Pro Val Ala Gly Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala
 65 70 75 80

His Glu Phe Thr Ala Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala
 85 90 95

Met Leu Pro Leu Leu Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val
 100 105 110

Thr Leu Ala Ala Asp Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg
 115 120 125

Ser Gly Ser Leu Glu Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn
 130 135 140

Arg Pro Ala Lys Ala Leu Leu Lys Gln Ala Gly His Ile Val Glu Val
 145 150 155 160

Gly Gly Asp Gly Thr Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu
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Val Leu Gly Asn Val Thr Leu Pro Lys Ala His
 180 185

<210> 775

<211> 1332

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1309)

<223> RXA01720

<400> 775

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 Val Ala Gln Gln Arg
 1 5

agc gtc gat gac tat ctt tcc att ttg ata gac agc gtc gca ccg ctt 163
 Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp Ser Val Ala Pro Leu
 10 15 20

ccg cca gta aaa acc cct atc ctc ggc gcg cat ccg tta agt cac ctt 211
 Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His Pro Leu Ser His Leu
 25 30 35

gca gag gat gtt gtc gcg aca att cct atc ccg aaa ttt act aat tct 259
 Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro Lys Phe Thr Asn Ser
 40 45 50

gct gtt gat ggt tac gcc att ttg aaa gaa gac atc cat ggc agc ggg 307
 Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp Ile His Gly Ser Gly
 55 60 65

ccg tgg aca ttt ctt gtg ggc ggt gat act ccg gcg ggt tct gcg ccg 355
 Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro Ala Gly Ser Ala Pro
 70 75 80 85

gcg agc att aat aat gga aaa gcc atc cgt gtg atg aca ggt gga ccc 403
 Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val Met Thr Gly Gly Pro
 90 95 100

gtc cca tcc acc aac aag gac atg atc gtg gtt cca gtg gag ctc acc	451
Val Pro Ser Thr Asn Lys Asp Met Ile Val Val Pro Val Glu Leu Thr	
105 110 115	
aat gct ccg gtg gat cac tcg ctt cct aca gaa atc acg atc aat gag	499
Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu Ile Thr Ile Asn Glu	
120 125 130	
cta cca ggt gag agg aat aat att cgc cat gct ggt gag cat ctt aaa	547
Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala Gly Glu His Leu Lys	
135 140 145	
gaa ggc gaa att gcg gtt gct gcg ggg acg gca ttt gat gcg ggt act	595
Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala Phe Asp Ala Gly Thr	
150 155 160 165	
gtg tcg acg gtg att tca gtt ggc cat gac act gta aaa gcc cat cct	643
Val Ser Thr Val Ile Ser Val Gly His Asp Thr Val Lys Ala His Pro	
170 175 180	
tgc cct ccg gtt gcg gtg atc act acc ggt gat gag cta aac cag gga	691
Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp Glu Leu Asn Gln Gly	
185 190 195	
aat ccc tgg ggt atc cct aat tcc aat ggg ccg atg ctg gtt gcg gag	739
Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro Met Leu Val Ala Glu	
200 205 210	
cta aaa cgc gtg ggg att aag gat ccg cag cat ttc cat tcc gat gat	787
Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His Phe His Ser Asp Asp	
215 220 225	
tct gag act gca ttg agg gag acg ctc gat aag cct gca gag gtt gcg	835
Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys Pro Ala Glu Val Ala	
230 235 240 245	
gat gtg atc atc act gtg ggt ggg atc tcg gcg ggc gcg ttc gat gtg	883
Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala Gly Ala Phe Asp Val	
250 255 260	
gtc aaa gcc gtg gga act aag act ggt ggt ttt gaa ttc ttc ccc att	931
Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe Glu Phe Phe Pro Ile	
265 270 275	
gcg atg aag ccg ggt aaa ccg caa ggt cat ggg cag tgg ggc gac gca	979
Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly Gln Trp Gly Asp Ala	
280 285 290	
aaa gtg gtg tgt ctg ccg gga aac ccg gtg gcg gcg tgg gtt agt ttt	1027
Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala Ala Trp Val Ser Phe	
295 300 305	
agg ctc ttt gtt gtt ccg gta att gag aga tta ggg ggt gga aag agg	1075
Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu Gly Gly Gly Lys Arg	
310 315 320 325	
ctg gcg tcg ata agc gaa ctc cct gtg gtg gcg ctg cgc tcg aac ccg	1123
Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala Leu Arg Ser Asn Arg	
330 335 340	
gcg ctg aag gcg ccg gag ggc ccc gta ttg gcg ata ccg gtg gcg att	1171

Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala Ile Pro Val Ala Ile
 345 350 355

gat tgg gag aaa aga atg gca aat tct cag gca cat cga tcc cat atg 1219
 Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala His Arg Ser His Met
 360 365 370

gtc ggt gca ctg gct gga agt ggc ggt att gca ctg gtg act tcg tcg 1267
 Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala Leu Val Thr Ser Ser
 375 380 385

att gcc gag gac ggt ctg gtt gat gtt gtg ctg ggg aga atg 1309
 Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu Gly Arg Met
 390 395 400

taaatagaata tcatcattct tgc 1332

<210> 776

<211> 403

<212> PRT

<213> Corynebacterium glutamicum ,

<400> 776

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Ser Val Ala Pro Leu Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His
 20 25 30

Pro Leu Ser His Leu Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro
 35 40 45

Lys Phe Thr Asn Ser Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp
 50 55 60

Ile His Gly Ser Gly Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro
 65 70 75 80

Ala Gly Ser Ala Pro Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val
 85 90 95

Met Thr Gly Gly Pro Val Pro Ser Thr Asn Lys Asp Met Ile Val Val
 100 105 110

Pro Val Glu Leu Thr Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu
 115 120 125

Ile Thr Ile Asn Glu Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala
 130 135 140

Gly Glu His Leu Lys Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala
 145 150 155 160

Phe Asp Ala Gly Thr Val Ser Thr Val Ile Ser Val Gly His Asp Thr
 165 170 175

Val Lys Ala His Pro Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp
 180 185 190

Glu Leu Asn Gln Gly Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro

195					200					205						
Met	Leu	Val	Ala	Glu	Leu	Lys	Arg	Val	Gly	Ile	Lys	Asp	Pro	Gln	His	
210					215					220						
Phe	His	Ser	Asp	Asp	Ser	Glu	Thr	Ala	Leu	Arg	Glu	Thr	Leu	Asp	Lys	
225					230					235					240	
Pro	Ala	Glu	Val	Ala	Asp	Val	Ile	Ile	Thr	Val	Gly	Gly	Ile	Ser	Ala	
245					250					255						
Gly	Ala	Phe	Asp	Val	Val	Lys	Ala	Val	Gly	Thr	Lys	Thr	Gly	Gly	Phe	
260					265					270						
Glu	Phe	Phe	Pro	Ile	Ala	Met	Lys	Pro	Gly	Lys	Pro	Gln	Gly	His	Gly	
275					280					285						
Gln	Trp	Gly	Asp	Ala	Lys	Val	Val	Cys	Leu	Pro	Gly	Asn	Pro	Val	Ala	
290					295					300						
Ala	Trp	Val	Ser	Phe	Arg	Leu	Phe	Val	Val	Pro	Val	Ile	Glu	Arg	Leu	
305					310					315					320	
Gly	Gly	Gly	Lys	Arg	Leu	Ala	Ser	Ile	Ser	Glu	Leu	Pro	Val	Val	Ala	
325					330					335						
Leu	Arg	Ser	Asn	Arg	Ala	Leu	Lys	Ala	Arg	Glu	Gly	Pro	Val	Leu	Ala	
340					345					350						
Ile	Pro	Val	Ala	Ile	Asp	Trp	Glu	Lys	Arg	Met	Ala	Asn	Ser	Gln	Ala	
355					360					365						
His	Arg	Ser	His	Met	Val	Gly	Ala	Leu	Ala	Gly	Ser	Gly	Gly	Ile	Ala	
370					375					380						
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385					390					395					400	
Gly Arg Met																

<210> 777

<211> 1237

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (2)..(1207)

<223> RXS03223

<400> 777

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1				5				10					15			

gcg	gaa	gag	gtt	caa	gct	agt	cgt	gct	ttg	ccg	ggt	ttc	gcg	caa	gca	97
Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Gly	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala
			20					25					30			

gcg att gat ggt tat gcg gtt cga gca gtc gat gtc ggc ggc gag aag	145
Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys	
35 40 45	
tcg ttt agc cag caa ctg ccg gtt gct cct ccg gaa aaa tcc ctg ccc	193
Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro	
50 55 60	
gtg gtg ggt gaa gta gct gcg ggt tct cag cag ccg ttg cgc ctg cag	241
Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln	
65 70 75 80	
cct aaa caa gca gtc atg gtc cac acc ggt gcg cca ctg ccg atg ctt	289
Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu	
85 90 95	
gcg gat gcg gtg ctg ccc atg gcg tgg tca gat cgt ggc cgc aaa cga	337
Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg	
100 105 110	
gta acc gcg cag cga cct gtg cgc tct ggc gag ttt gtg cgc aaa gaa	385
Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu	
115 120 125	
ggc gat gac atc caa ccg gga gac atc gca gtc agc gcc ggc gcg gtc	433
Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val	
130 135 140	
tta ggc cct gcc caa att ggt ttg ctc gca gct gtt ggt cgc tcc aaa	481
Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys	
145 150 155 160	
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Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala	
165 170 175	
gaa ctt gtt gat att gat cgc cag cca ggc ctc ggc cag gtt tat gat	577
Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp	
180 185 190	
gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat	625
Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp	
195 200 205	
gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag	673
Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu	
210 215 220	
atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga	721
Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly	
225 230 235 240	
gct gtt ggc ggt gct ggt tca gct ggc gtg cgc cag gtt ctc aac gag	769
Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu	
245 250 255	
cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc	817
Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val	
260 265 270	
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg	865

Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu
 275 280 285

cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc 913
 Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg
 290 295 300

ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt 961
 Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val
 305 310 315 320

gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa 1009
 Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys
 325 330 335

ggc ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac 1057
 Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr
 340 345 350

ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg 1105
 Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu
 355 360 365

gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc 1153
 Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val
 370 375 380

aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa 1201
 Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
 385 390 395 400

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 Gly Arg

<210> 778

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 778

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 20 25 30

Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys
 35 40 45

Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro
 50 55 60

Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln
 65 70 75 80

Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu
 85 90 95

Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg

100					105					110					
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu
		115						120						125	
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val
	130						135					140			
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys
145					150					155					160
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala
				165					170					175	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp
			180					185					190		
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp
		195					200					205			
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu
	210					215					220				
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly
225					230					235					240
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu
				245					250					255	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val
			260					265					270		
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu
		275					280					285			
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg
		290				295					300				
Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val
305					310					315					320
Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys
				325					330					335	
Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr
			340					345					350		
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu
		355					360					365			
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val
	370					375					380				
Thr	Glu	Ile	Arg	Pro	Gly	Asp	Val	Val	Asp	Val	Ile	Phe	Leu	Ala	Gln
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Gly	Arg														

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<211> 1229
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1206)
 <223> FRXA01970

<400> 779

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Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala	
20 25 30	
gcg att gat ggt tat gcg gtt cga gca gtc gat gtc ggc ggc gag aag	144
Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys	
35 40 45	
tcg ttt agc cag caa ctg ccg gtt gct cct ccg gaa aaa tcc ctg ccc	192
Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro	
50 55 60	
gtg gtg ggt gaa gta gct gcg ggt tct cag cag ccg ttg cgc ctg cag	240
Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln	
65 70 75 80	
cct aaa caa gca gtc atg gtc cac acc ggt gcg cca ctg ccg atg ctt	288
Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu	
85 90 95	
gcg gat gcg gtg ctg ccc atg gcg tgg tca gat cgt ggc cgc aaa cga	336
Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg	
100 105 110	
gta acc gcg cag cga cct gtg cgc tct ggc gag ttt gtg cgc aaa gaa	384
Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu	
115 120 125	
ggc gat gac atc caa ccg gga gac atc gca gtc agc gcc ggc gcg gtc	432
Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val	
130 135 140	
tta ggc cct gcc caa att ggt ttg ctc gca gct gtt ggt cgc tcc aaa	480
Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys	
145 150 155 160	
gtg ttg gtg tac cca cgc cca cgc atg tcg gtt atc tcc gta ggc gct	528
Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala	
165 170 175	
gaa ctt gtt gat att gat cgc cag cca ggc ctc ggc cag gtt tat gat	576
Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp	
180 185 190	
gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat	624
Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp	
195 200 205	


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gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag 672
Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu
210 215 220

atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga 720
Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly
225 230 235 240

gct gtt ggc ggt gct ggt tca gct ggc gtg cgc cag gtt ctc aac gag 768
Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu
245 250 255

cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc 816
Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val
260 265 270

caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg 864
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu
275 280 285

cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc 912
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg
290 295 300

ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt 960
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val
305 310 315 320

gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa 1008
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys
325 330 335

ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac 1056
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr
340 345 350

ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg 1104
Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu
355 360 365

gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc 1152
Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val
370 375 380

aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa 1200
Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
385 390 395 400

ggt cga tagttcgatg cgtaatgcac cgt 1229
Gly Arg

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<210> 780

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 780

Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys

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Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala	20	25	30
Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys	35	40	45
Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro	50	55	60
Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln	65	70	75
Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu	85	90	95
Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg	100	105	110
Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu	115	120	125
Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val	130	135	140
Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys	145	150	155
Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala	165	170	175
Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp	180	185	190
Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp	195	200	205
Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu	210	215	220
Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly	225	230	235
Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu	245	250	255
Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val	260	265	270
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu	275	280	285
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg	290	295	300
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val	305	310	315
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys	325	330	335

Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr
 340 345 350

Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu
 355 360 365

Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val
 370 375 380

Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
 385 390 395 400

Gly Arg

<210> 781
 <211> 708
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(685)
 <223> RXA02629

<400> 781
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atctgcatct aatcaagtag ccaagtatga gtgaggaaca atg agc aag gat cca 115
 Met Ser Lys Asp Pro
 1 5

ttg gga agt ctt acc gat gtt gta gac aca cga gtt ccg ctt ccg gat 163
 Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg Val Pro Leu Pro Asp
 10 15 20

gtt gaa ccg gat ccg gag ttc ctg aag gct acg gaa aaa gaa ttc cac 211
 Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr Glu Lys Glu Phe His
 25 30 35

atg gca tcc cag aag cgc gct ctt gtt gtc ctg gtg ggc gat cat gtc 259
 Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu Val Gly Asp His Val
 40 45 50

gct gag gca gat ggg act ggc cgt ttg gtt acg gag ctg ctc tta gag 307
 Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr Glu Leu Leu Leu Glu
 55 60 65

tct ggc ttc aac gtg gac gct gtg gtc agc gtg aag tct aag aag tct 355
 Ser Gly Phe Asn Val Asp Ala Val Val Ser Val Lys Ser Lys Lys Ser
 70 75 80 85

cag att agg caa gct att gaa acc gca gtt gtt ggc ggc gct gac ctt 403
 Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val Gly Gly Ala Asp Leu
 90 95 100

gtg ctg acc atc ggc gga gtg ggc gtt ggt cct cgg gat aaa act cct 451
 Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro Arg Asp Lys Thr Pro
 105 110 115

gag gca acc agc gct gtg ttg gac cag gac gtc cca gga atc gcg cag 499
 Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val Pro Gly Ile Ala Gln
 120 125 130
 gcg ctt cgt tcc tcc ggt ttg gcc tgt ggc gcg gtg gat gca agt gtt 547
 Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala Val Asp Ala Ser Val
 135 140 145
 tcc cga ggc gta gcg ggc gta tcc ggc tca acc gtg gtg gtc aac ctc 595
 Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr Val Val Val Asn Leu
 150 155 160 165
 gct gag tct cgt tcc gca att cgt gat ggc atg gca act ctg aca ccg 643
 Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met Ala Thr Leu Thr Pro
 170 175 180
 ttg gtt gat ttt gtt gta gat cag ctt cgc act tcc gtg gtt 685
 Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr Ser Val Val
 185 190 195
 tgagttggtc gggtgtgagt aga 708

<210> 782

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 782

Met Ser Lys Asp Pro Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg
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 20 25 30
 Glu Lys Glu Phe His Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu
 35 40 45
 Val Gly Asp His Val Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr
 50 55 60
 Glu Leu Leu Leu Glu Ser Gly Phe Asn Val Asp Ala Val Val Ser Val
 65 70 75 80
 Lys Ser Lys Lys Ser Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val
 85 90 95
 Gly Gly Ala Asp Leu Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro
 100 105 110
 Arg Asp Lys Thr Pro Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val
 115 120 125
 Pro Gly Ile Ala Gln Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala
 130 135 140
 Val Asp Ala Ser Val Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr
 145 150 155 160
 Val Val Val Asn Leu Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met

	165		170		175
Ala Thr Leu Thr Pro Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr					
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Ser Val Val					
	195				

<210> 783
 <211> 402
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(379)
 <223> RXA02318

<400> 783
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 cagtaagcgc atgtgcgcca ttttaaggca agatggggcc atg aat tcg ctt ttc 115
 Met Asn Ser Leu Phe
 1 5
 gac gtc tcc cca cac tgg tcc tcc gcc aac gcc aag ctc acc gca cat 163
 Asp Val Ser Pro His Trp Ser Ser Ala Asn Ala Lys Leu Thr Ala His
 10 15 20
 ttt aac acc gga aaa ttc tcc act ggc atg aaa ttt gtc aac ctc att 211
 Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys Phe Val Asn Leu Ile
 25 30 35
 gcc gac tcc gca gaa gaa gcc aac cac cac ccc gat atc ctt ctc acc 259
 Ala Asp Ser Ala Glu Glu Ala Asn His His Pro Asp Ile Leu Leu Thr
 40 45 50
 tat ggt ttt gtg gaa atc acc ctc acc agc cac gat gtg ggt gag ata 307
 Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His Asp Val Gly Glu Ile
 55 60 65
 acc gac cgt gat gtc gcc cta gca aaa gtc atc gac gcc cac gcc aag 355
 Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile Asp Ala His Ala Lys
 70 75 80 85
 acc ttg gcc att tcg gca gag gct taagggtaaa gattatgagc aac 402
 Thr Leu Ala Ile Ser Ala Glu Ala
 90

<210> 784
 <211> 93
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 784
 Met Asn Ser Leu Phe Asp Val Ser Pro His Trp Ser Ser Ala Asn Ala
 1 5 10 15
 Lys Leu Thr Ala His Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys

	20		25		30
Phe Val Asn Leu Ile Ala Asp Ser Ala Glu Glu Ala Asn His His Pro	35	40	45		
Asp Ile Leu Leu Thr Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His	50	55	60		
Asp Val Gly Glu Ile Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile	65	70	75	80	
Asp Ala His Ala Lys Thr Leu Ala Ile Ser Ala Glu Ala	85	90			

<210> 785

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> RXA01517

<400> 785

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gttccaggaa atccatggct gctggaagga gcaacgccta atg cat gca gtt ttg 115
                                     Met His Ala Val Leu
                                     1 5

tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg 163
Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val
                                     10 15 20

atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca 211
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser
                                     25 30 35

acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg 259
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val
                                     40 45 50

ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc 307
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly
                                     55 60 65

caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg 355
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly
                                     70 75 80 85

cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa 403
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu
                                     90 95 100

gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct 451
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala
                                     105 110 115

tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat 499

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Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp
      120              125              130

gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat   547
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp
      135              140              145

ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat   597
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile
      150              155

gca                                                                    600

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<210> 786

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 786

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Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln
      20              25              30

Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu
      35              40              45

Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu
      50              55              60

Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg
      65              70              75              80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile
      85              90              95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu
      100             105             110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu
      115             120             125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His
      130             135             140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile
      145             150             155

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<210> 787

<211> 609

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(586)

<223> RXN01304

<400> 787

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tgaaaaaggg gattaattac cccacttga ggagaaattg atg ccc gca cag aac 115
                                         Met Pro Ala Gln Asn
                                         1 5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163
Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser
                        10 15 20

gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag 211
Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln
                        25 30 35

gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt 259
Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe
                        40 45 50

gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc 307
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg
                        55 60 65

gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg 355
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr
                        70 75 80 85

ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg 403
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met
                        90 95 100

acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta 451
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu
                        105 110 115

tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc 499
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu
                        120 125 130

atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg 547
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly
                        135 140 145

gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagattt 596
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu
                        150 155 160

ttgcttatcg acg 609

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<210> 788

<211> 162

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 788

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Asp Arg Ile Lys Ser Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala
  20 25 30

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[illegible]

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<210> 789
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1258)
<223> RXS02556
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<400> 789																
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gtagaaatta gcccatgaag catggaaagg cgaaaacccc							ttg	atc	gtt	tcc	acc	115				
							Leu	Ile	Val	Ser	Thr					
							1				5					
cag	ccc	att	act	gat	cgc	agc	gca	ctc	tcg	gca	gaa	cac	gca	gag	gtg	163
Gln	Pro	Ile	Thr	Asp	Arg	Ser	Ala	Leu	Ser	Ala	Glu	His	Ala	Glu	Val	
				10					15					20		
atc	aaa	gca	acg	ctt	cct	ctc	gtg	ggc	ggc	aag	att	aat	gag	atc	acg	211
Ile	Lys	Ala	Thr	Leu	Pro	Leu	Val	Gly	Gly	Lys	Ile	Asn	Glu	Ile	Thr	
				25					30					35		
ccg	gtt	ttc	tac	aac	aag	atg	ttt	gcg	gct	cac	cca	gaa	ttg	atc	gct	259
Pro	Val	Phe	Tyr	Asn	Lys	Met	Phe	Ala	Ala	His	Pro	Glu	Leu	Ile	Ala	
				40					45					50		
aac	acc	ttc	aac	cgt	ggc	aat	cag	aag	caa	ggc	gat	cag	cag	aag	gcg	307
Asn	Thr	Phe	Asn	Arg	Gly	Asn	Gln	Lys	Gln	Gly	Asp	Gln	Gln	Lys	Ala	
				55					60					65		

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat	355
Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp	
70 75 80 85	
gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg	403
Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val	
90 95 100	
tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg	451
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu	
105 110 115	
ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct	499
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro	
120 125 130	
gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg	547
Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu	
135 140 145	
atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc	595
Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly	
150 155 160 165	
gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca	643
Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala	
170 175 180	
acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca	691
Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro	
185 190 195	
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag	739
Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln	
200 205 210	
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att	787
Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile	
215 220 225	
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta	835
Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val	
230 235 240 245	
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt	883
Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val	
250 255 260	
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc	931
Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly	
265 270 275	
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac	979
Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp	
280 285 290	
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg	1027
Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val	
295 300 305	

gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa 1075
 Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu
 310 315 320 325
 atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att 1123
 Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile
 330 335 340
 cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag 1171
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys
 345 350 355
 aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta 1219
 Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val
 360 365 370
 aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca 1268
 Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser
 375 380 385
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<210> 790

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 790

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 35 40 45
 Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly
 50 55 60
 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95
 Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
 100 105 110
 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu
 180 185 190
 Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
 195 200 205
 Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
 210 215 220
 Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
 225 230 235 240
 Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
 245 250 255
 Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
 260 265 270
 Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
 275 280 285
 Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
 290 295 300
 Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
 305 310 315 320
 Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
 325 330 335
 Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
 340 345 350
 Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
 355 360 365
 Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
 370 375 380
 Ile Ser
 385

<210> 791

<211> 990

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(967)

<223> RXS02560

<400> 791

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 Met Gln Gly Asn Ser

1

5

ctt	aat	ctg	gca	gac	aac	agc	gag	aga	aag	aag	ccc	atg	ccg	tca	cca	163
Leu	Asn	Leu	Ala	Asp	Asn	Ser	Glu	Arg	Lys	Lys	Pro	Met	Pro	Ser	Pro	
				10					15					20		
gga	gaa	ctt	tta	gcc	gcc	cgc	tac	gga	caa	cct	gca	acc	tgg	acg	cca	211
Gly	Glu	Leu	Leu	Ala	Ala	Arg	Tyr	Gly	Gln	Pro	Ala	Thr	Trp	Thr	Pro	
			25					30					35			
ccg	cag	tgg	aat	gag	acg	ctt	gat	gtc	att	cac	cag	cat	cga	tca	gtt	259
Pro	Gln	Trp	Asn	Glu	Thr	Leu	Asp	Val	Ile	His	Gln	His	Arg	Ser	Val	
		40					45					50				
cgc	agg	tgg	ttg	gat	aaa	ccg	gtt	gat	gat	gac	acc	atc	cgc	acc	att	307
Arg	Arg	Trp	Leu	Asp	Lys	Pro	Val	Asp	Asp	Asp	Thr	Ile	Arg	Thr	Ile	
	55					60					65					
att	tcc	gcc	gca	caa	tcg	gct	gga	acc	tct	tcc	aat	aag	cag	gtc	att	355
Ile	Ser	Ala	Ala	Gln	Ser	Ala	Gly	Thr	Ser	Ser	Asn	Lys	Gln	Val	Ile	
	70				75					80					85	
tct	gtc	atc	gtg	gtt	aaa	gat	cct	gag	ctg	agg	aaa	ggc	ctc	gcg	ggg	403
Ser	Val	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Arg	Lys	Gly	Leu	Ala	Gly	
				90					95					100		
atc	act	cgc	cag	atg	ttt	ccg	cac	ctt	gag	cag	gtt	ccc	gcg	gtg	ctg	451
Ile	Thr	Arg	Gln	Met	Phe	Pro	His	Leu	Glu	Gln	Val	Pro	Ala	Val	Leu	
			105					110					115			
att	tgg	ttg	att	gat	tat	tcc	cga	atc	agt	gcg	gtg	gca	gcc	aga	gaa	499
Ile	Trp	Leu	Ile	Asp	Tyr	Ser	Arg	Ile	Ser	Ala	Val	Ala	Ala	Arg	Glu	
		120					125					130				
gat	ctc	cca	aca	ggg	gct	ctt	gat	tat	ctc	gat	gag	gcc	gcg	tgg	ggg	547
Asp	Leu	Pro	Thr	Gly	Ala	Leu	Asp	Tyr	Leu	Asp	Glu	Ala	Ala	Trp	Gly	
	135					140				145						
ttc	ctc	gac	gcc	gga	atc	gca	gct	caa	aac	gct	gca	att	gct	gcg	gag	595
Phe	Leu	Asp	Ala	Gly	Ile	Ala	Ala	Gln	Asn	Ala	Ala	Ile	Ala	Ala	Glu	
	150				155				160						165	
tca	ctt	gga	ttg	gga	acg	ctc	tat	ttg	ggc	tcg	gtg	cgc	aac	gat	gcg	643
Ser	Leu	Gly	Leu	Gly	Thr	Leu	Tyr	Leu	Gly	Ser	Val	Arg	Asn	Asp	Ala	
				170					175					180		
gaa	gcc	gtg	cac	aaa	ttg	ctt	ggc	ctt	cca	cct	gag	atc	gtg	cct	gtc	691
Glu	Ala	Val	His	Lys	Leu	Leu	Gly	Leu	Pro	Pro	Glu	Ile	Val	Pro	Val	
			185					190					195			
gtg	ggc	ttg	gaa	atg	ggg	cat	gcg	gat	ccg	cct	gaa	cct	gcc	gga	att	739
Val	Gly	Leu	Glu	Met	Gly	His	Ala	Asp	Pro	Pro	Glu	Pro	Ala	Gly	Ile	
		200					205					210				
aaa	cct	ccc	ctg	cca	caa	gaa	gcc	att	gtt	cac	tgg	gat	acc	tac	acc	787
Lys	Pro	Pro	Leu	Pro	Gln	Glu	Ala	Ile	Val	His	Trp	Asp	Thr	Tyr	Thr	
	215					220					225					
gag	aaa	aac	ctc	gaa	ctt	atc	gat	tcc	tac	gac	cgc	gcc	ctc	gac	act	835
Glu	Lys	Asn	Leu	Glu	Leu	Ile	Asp	Ser	Tyr	Asp	Arg	Ala	Leu	Asp	Thr	
	230				235					240					245	
tac	tat	tct	cgc	tac	ggc	cag	cac	cag	ctc	tgg	tcg	aag	cag	acg	gcg	883

Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
 250 255 260
 cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
 265 270 275
 agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
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 attatggacg cct 990

<210> 792

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 792

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 35 40 45
 Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60
 Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80
 Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95
 Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110
 Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125
 Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140
 Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160
 Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175
 Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190
 Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205
 Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
 225 230 235 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
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Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr
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Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu
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Arg

<210> 793
 <211> 1425
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1402)
 <223> RXA00382

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ctggattggc ttcacagatt gaattaatac aatgacgcac atg aca tcg tcc aat 115
 Met Thr Ser Ser Asn
 1 5

acg gct cga tcc gca gag tgg ttt gaa aag gct cag aag ctc acc cct 163
 Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala Gln Lys Leu Thr Pro
 10 15 20

ggg ggt gtg aat tct cct gtt cgc gct ttc ggt tca gtt ggc gga caa 211
 Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly Ser Val Gly Gly Gln
 25 30 35

gcc cgt ttc atc gaa aaa gct cac ggt tca acg ctg atc gat gtg gac 259
 Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr Leu Ile Asp Val Asp
 40 45 50

gga aat gaa tac gtt gac ctg gtc tgt tct tgg ggc ccc atg ctg atg 307
 Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp Gly Pro Met Leu Met
 55 60 65

ggg cac gct cac cca gca gtg gtc gag gct gtg cag aag gcc gtc gtg 355
 Gly His Ala His Pro Ala Val Val Glu Ala Val Gln Lys Ala Val Val
 70 75 80 85

gat ggt ctt tct ttc ggc gct ccc acc atc ggt gag gtt gag ttg gcc 403
 Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly Glu Val Glu Leu Ala
 90 95 100

caa gat atc gtc aag cgc act tct gtg gag gaa gtc cgc ctg gtc aac 451
 Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu Val Arg Leu Val Asn
 105 110 115

tcc ggc act gag gcc acc atg tcg gcg gtt cgt ctg gcg cgc ggt tac	499
Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg Leu Ala Arg Gly Tyr	
120 125 130	
act cag cgt tcc aag att ttg aag ttt gag ggc tgc tac cac ggc cac	547
Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly Cys Tyr His Gly His	
135 140 145	
gtc gat gcg ctg ctc gca tct gct ggt tct ggt gtc gca act ttc gct	595
Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly Val Ala Thr Phe Ala	
150 155 160 165	
ctg cct gat tcc cca ggc atc acc ggc gct cag act tct gac act att	643
Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln Thr Ser Asp Thr Ile	
170 175 180	
gtt gtt cct tac aac gac att gaa gcc gtg cgc aac gct ttt gcg gag	691
Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg Asn Ala Phe Ala Glu	
185 190 195	
tac cca ggc gag atc gcc tgc atc atc gca gag gca gcc ggt ggc aac	739
Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu Ala Ala Gly Gly Asn	
200 205 210	
atg ggc acc gtc gct cca aag gac aac ttt aac gac aag ctt ctc gcg	787
Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn Asp Lys Leu Leu Ala	
215 220 225	
atc gct cac gct gac ggc gcg ctg ctg atc ctc gat gaa gtc atg acc	835
Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu Asp Glu Val Met Thr	
230 235 240 245	
ggc ttc cgc acc tct tac cgt ggc tgg ttc ggc gta gac aag gtt gcc	883
Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly Val Asp Lys Val Ala	
250 255 260	
gct gac ctg gtc acc ttc ggc aag gtc gtc tcc ggc ggc cta cct gcc	931
Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser Gly Gly Leu Pro Ala	
265 270 275	
gca gcg ttt ggc ggc aag gct gaa atc atg aac atg ctg gcc cca cag	979
Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn Met Leu Ala Pro Gln	
280 285 290	
ggc ccc gtc tac caa gca ggc aca ctg tcc ggc aac ccg gtt gcg gtc	1027
Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly Asn Pro Val Ala Val	
295 300 305	
gca gct ggt cgg gca tcg ctt aag ctt gcc gac gaa tcc ctc tac aca	1075
Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp Glu Ser Leu Tyr Thr	
310 315 320 325	
acc atc aac gcc aac gca gat cgt ctc cac ggt ttg atc tct gat gcc	1123
Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly Leu Ile Ser Asp Ala	
330 335 340	
tta acc cac gaa ggc gta gcc cac cac att cag cgt gcc tca aac atg	1171
Leu Thr His Glu Gly Val Ala His His Ile Gln Arg Ala Ser Asn Met	
345 350 355	


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<210> 794
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<212> PRT
<213> Corynebacterium glutamicum

<400> 794
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Gln Lys Leu Thr Pro Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly
      20          25          30
Ser Val Gly Gly Gln Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr
      35          40          45
Leu Ile Asp Val Asp Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp
      50          55          60
Gly Pro Met Leu Met Gly His Ala His Pro Ala Val Val Glu Ala Val
      65          70          75          80
Gln Lys Ala Val Val Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly
      85          90          95
Glu Val Glu Leu Ala Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu
      100          105          110
Val Arg Leu Val Asn Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg
      115          120          125
Leu Ala Arg Gly Tyr Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly
      130          135          140
Cys Tyr His Gly His Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly
      145          150          155          160
Val Ala Thr Phe Ala Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln
      165          170          175

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Thr Ser Asp Thr Ile Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg
 180 185 190
 Asn Ala Phe Ala Glu Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu
 195 200 205
 Ala Ala Gly Gly Asn Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn
 210 215 220
 Asp Lys Leu Leu Ala Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu
 225 230 235 240
 Asp Glu Val Met Thr Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly
 245 250 255
 Val Asp Lys Val Ala Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser
 260 265 270
 Gly Gly Leu Pro Ala Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn
 275 280 285
 Met Leu Ala Pro Gln Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly
 290 295 300
 Asn Pro Val Ala Val Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp
 305 310 315 320
 Glu Ser Leu Tyr Thr Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly
 325 330 335
 Leu Ile Ser Asp Ala Leu Thr His Glu Gly Val Ala His His Ile Gln
 340 345 350
 Arg Ala Ser Asn Met Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His
 355 360 365
 Asn Phe Ser Asp Met Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe
 370 375 380
 Phe His Thr Leu Leu Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe
 385 390 395 400
 Glu Thr Trp Phe Val Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys
 405 410 415
 Ile Glu Gln Ala Leu Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys
 420 425 430

Ala Ser

<210> 795
 <211> 1233
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1210)

<400> 795

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tcg	gat	gca	ttt	gac	gcc	ctc	ctt	gtg	ctc	tcc	ttc	ggg	ggg	ccc	gaa	163
Ser	Asp	Ala	Phe	Asp	Ala	Leu	Leu	Val	Leu	Ser	Phe	Gly	Gly	Pro	Glu	
				10					15					20		

ggg cac gag gag gtt cgt ccg ttt ttg gag aat gtc act cac gga agg 211
Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn Val Thr His Gly Arg
25 30 35

ggg att ccg ccg gaa cgt cta gat gaa gtg gcg gtt cat tac cac cac 259
Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala Val His Tyr His His
40 45 50

ttc ggt ggt atc agc ccc atc aat gcg ctg aac agg gaa att atc gcc 307
Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn Arg Glu Ile Ile Ala
55 60 65

aat gtg gaa aaa gaa ttg gcg tct cgc gat cac aag ctg cct gtt tat 355
Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His Lys Leu Pro Val Tyr
70 75 80 85

ttt ggt aac cgc aac tgg aag ccg ttt gat aat gag gcc gct gaa caa 403
Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn Glu Ala Ala Glu Gln
90 95 100

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atg gct gat gac ggc gtg aaa aac gcg ctg gtg ttg gca act tcc gct    451
Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val Leu Ala Thr Ser Ala
      105                      110                      115

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tgg ggt ggc tac tcc ggt tgt cgg cag tac cag gaa gat att cag ggc 499
 Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln Glu Asp Ile Gln Gly
 120 125 130

atg atc aag cac ctg gag tct cag ggg cag tcg atc acg ttc acc aag 547
Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser Ile Thr Phe Thr Lys
135 140 145

ctg cgt cag ttc tac gat cac cct cgt ttt gtc tcc acc atg gct caa 595
Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val Ser Thr Met Ala Gln
150 155 160 165

ttg gtt cag gat tcc tac gcg aag ctt ccc gat gag ctg cga gat gag	643
Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp Glu Leu Arg Asp Glu	
170 175 180	

gcg cgt ctg gtc ttc acc gcg cac tcc att cca ctg act gcg gac aat 691
Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro Leu Thr Ala Asp Asn
185 190 195

gct gcg gga acc cct gag gat ggc tcc ttg tat tcc aca cag gtc aag 739
Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr Ser Thr Gln Val Lys
200 205 210

gaa gcg tca gca ctg att gct gag gct gtt ggt gtg tca gat ttt gat 787
 Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly Val Ser Asp Phe Asp
 215 220 225

gtg gtg tgg cag tcc cgc tcg ggt agc ccg cac act ccg tgg ctg gag 835
 Val Val Trp Gln Ser Arg Ser Gly Ser Pro His Thr Pro Trp Leu Glu
 230 235 240 245

cct gac atc gtg gat cac gca gtg gag ctc aac gag aag ggt caa aaa 883
 Pro Asp Ile Val Asp His Ala Val Glu Leu Asn Glu Lys Gly Gln Lys
 250 255 260

gcg ctc gtt gtc tgc cct gta ggc ttt att tct gat cat atg gaa gtc 931
 Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser Asp His Met Glu Val
 265 270 275

att tgg gat ctt gat tcc gag ctg atg gaa gaa gcc gag aag cgc aac 979
 Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu Ala Glu Lys Arg Asn
 280 285 290

atg gtg gtc gag cgt gtc gct acc gtt ggc ccc acc gat gaa ttc gca 1027
 Met Val Val Glu Arg Val Ala Thr Val Gly Pro Thr Asp Glu Phe Ala
 295 300 305

gcc ctt gtg gtt gat ctc atc gag gag gca gag ctc aag cgc gtt atc 1075
 Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu Leu Lys Arg Val Ile
 310 315 320 325

gag cgc ctt gga aag ctg cca gca cgc gga agt tcc gtc aac ggc gca 1123
 Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser Ser Val Asn Gly Ala
 330 335 340

ccg tgt ggc gac ggc tgc tgt ggt acc gcc aag cat aaa acc gcg cgg 1171
 Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys His Lys Thr Ala Arg
 345 350 355

gtg aac ccc aac gct cgc tca gcg gcg cca gct gcc aac taggagtgat 1220
 Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala Ala Asn
 360 365 370

agtcctcgc aaa 1233

<210> 796

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 796

Met Asn Glu Arg Thr Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser
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Phe Gly Gly Pro Glu Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn
 20 25 30

Val Thr His Gly Arg Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala
 35 40 45

Val His Tyr His His Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn
 50 55 60

Arg	Glu	Ile	Ile	Ala	Asn	Val	Glu	Lys	Glu	Leu	Ala	Ser	Arg	Asp	His	65	70	75	80
Lys	Leu	Pro	Val	Tyr	Phe	Gly	Asn	Arg	Asn	Trp	Lys	Pro	Phe	Asp	Asn	85	90	95	
Glu	Ala	Ala	Glu	Gln	Met	Ala	Asp	Asp	Gly	Val	Lys	Asn	Ala	Leu	Val	100	105	110	
Leu	Ala	Thr	Ser	Ala	Trp	Gly	Gly	Tyr	Ser	Gly	Cys	Arg	Gln	Tyr	Gln	115	120	125	
Glu	Asp	Ile	Gln	Gly	Met	Ile	Lys	His	Leu	Glu	Ser	Gln	Gly	Gln	Ser	130	135	140	
Ile	Thr	Phe	Thr	Lys	Leu	Arg	Gln	Phe	Tyr	Asp	His	Pro	Arg	Phe	Val	145	150	155	160
Ser	Thr	Met	Ala	Gln	Leu	Val	Gln	Asp	Ser	Tyr	Ala	Lys	Leu	Pro	Asp	165	170	175	
Glu	Leu	Arg	Asp	Glu	Ala	Arg	Leu	Val	Phe	Thr	Ala	His	Ser	Ile	Pro	180	185	190	
Leu	Thr	Ala	Asp	Asn	Ala	Ala	Gly	Thr	Pro	Glu	Asp	Gly	Ser	Leu	Tyr	195	200	205	
Ser	Thr	Gln	Val	Lys	Glu	Ala	Ser	Ala	Leu	Ile	Ala	Glu	Ala	Val	Gly	210	215	220	
Val	Ser	Asp	Phe	Asp	Val	Val	Trp	Gln	Ser	Arg	Ser	Gly	Ser	Pro	His	225	230	235	240
Thr	Pro	Trp	Leu	Glu	Pro	Asp	Ile	Val	Asp	His	Ala	Val	Glu	Leu	Asn	245	250	255	
Glu	Lys	Gly	Gln	Lys	Ala	Leu	Val	Val	Cys	Pro	Val	Gly	Phe	Ile	Ser	260	265	270	
Asp	His	Met	Glu	Val	Ile	Trp	Asp	Leu	Asp	Ser	Glu	Leu	Met	Glu	Glu	275	280	285	
Ala	Glu	Lys	Arg	Asn	Met	Val	Val	Glu	Arg	Val	Ala	Thr	Val	Gly	Pro	290	295	300	
Thr	Asp	Glu	Phe	Ala	Ala	Leu	Val	Val	Asp	Leu	Ile	Glu	Glu	Ala	Glu	305	310	315	320
Leu	Lys	Arg	Val	Ile	Glu	Arg	Leu	Gly	Lys	Leu	Pro	Ala	Arg	Gly	Ser	325	330	335	
Ser	Val	Asn	Gly	Ala	Pro	Cys	Gly	Asp	Gly	Cys	Cys	Gly	Thr	Ala	Lys	340	345	350	
His	Lys	Thr	Ala	Arg	Val	Asn	Pro	Asn	Ala	Arg	Ser	Ala	Ala	Pro	Ala	355	360	365	
Ala	Asn															370			

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(787)
 <223> RXA00624

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 Met Ser Gly Arg Leu
 1 5
 ctt gtt tca gtt tct agt att ttc gac cag acc cga tcg gcg gct gac 163
 Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr Arg Ser Ala Ala Asp
 10 15 20
 agg ctc att tca gac ctg cga gcc gac ggc atc gag gtc tca tta ctt 211
 Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile Glu Val Ser Leu Leu
 25 30 35
 gtc gca ccc cgc atc gat ggg gac tgg cgt ctc gcc aaa gac aaa ggg 259
 Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu Ala Lys Asp Lys Gly
 40 45 50
 acc ctc gcg tgg atg gaa caa caa cgc gaa cgc ggc cac gaa ctc atc 307
 Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg Gly His Glu Leu Ile
 55 60 65
 ctc aac ggt ttc gac caa gca gtt cag gga cgt cgc tca gaa ttc gcc 355
 Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg Arg Ser Glu Phe Ala
 70 75 80 85
 aac ctt gaa cgg cac gaa gca cgt ctt cgc ctt acc ggt gcc att agg 403
 Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu Thr Gly Ala Ile Arg
 90 95 100
 caa atg cag aaa att ggc ttc gaa ttc caa atc ttt gcc cca cct cgt 451
 Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile Phe Ala Pro Pro Arg
 105 110 115
 tgg aga atg tca gaa ggc acc ttc gcg gta ctc cca gaa ttt gat ttc 499
 Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu Pro Glu Phe Asp Phe
 120 125 130
 aac gtc gcc gcc tcg acc agg gga tta cat aac ctc gac acc ggc gaa 547
 Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn Leu Asp Thr Gly Glu
 135 140 145
 ttc ttg gcg tgt aga aac ctc tcc gtg ggt gaa ggt ttt ggt gct gca 595
 Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu Gly Phe Gly Ala Ala
 150 155 160 165
 aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa 643
 Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu
 170 175 180

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aaa gga aat aca gtg cgc ttg tcc gca tcg gcg cga aat ctc acc aac 691
Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn
      185                      190                      195

cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat 739
Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala Leu Ala Ala Leu Asp
      200                      205                      210

ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc 787
Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala Ala Ala Gln Leu Ala
      215                      220                      225

tagttgggga ggttcggggc acc 810

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<210> 798

<211> 229

<212> PRT

<213> Corynebacterium glutamicum

<400> 798

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Met Ser Gly Arg Leu Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr
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Arg Ser Ala Ala Asp Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile
      20                      25                      30

Glu Val Ser Leu Leu Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu
      35                      40                      45

Ala Lys Asp Lys Gly Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg
      50                      55                      60

Gly His Glu Leu Ile Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg
      65                      70                      75                      80

Arg Ser Glu Phe Ala Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu
      85                      90                      95

Thr Gly Ala Ile Arg Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile
      100                      105                      110

Phe Ala Pro Pro Arg Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu
      115                      120                      125

Pro Glu Phe Asp Phe Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn
      130                      135                      140

Leu Asp Thr Gly Glu Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu
      145                      150                      155                      160

Gly Phe Gly Ala Ala Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val
      165                      170                      175

Thr Arg Gly Ala Glu Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala
      180                      185                      190

Arg Asn Leu Thr Asn Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala
      195                      200                      205

Leu Ala Ala Leu Asp Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala

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210 215 220

Ala Ala Gln Leu Ala
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<222> (1)..(933)
<223> RXA00306

<400> 799

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ggt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg	96
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val	
20 25 30	
gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat	144
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp	
35 40 45	
cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	
ggt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa	480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu	
145 150 155 160	
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag	528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln	
165 170 175	

tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc 576
 Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190
 acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc 624
 Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205
 ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat 672
 Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220
 gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc 720
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240
 acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc 768
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255
 atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg 816
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270
 gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285
 ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300
 ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag 956
 Pro Ala Asp Leu Leu Asp Ser
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<210> 800

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 800

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
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 20 25 30
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95

Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125
 Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140
 Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160
 Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175
 Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190
 Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205
 Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
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 Pro Ala Asp Leu Leu Asp Ser
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1240)
 <223> RXA00884

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 Met Ser Val Phe Gly
 1 5
 gtg tat att cat gtg ccg ttt tgt tca act cgg tgc ggt tat tgc gat 163

Val	Tyr	Ile	His	Val	Pro	Phe	Cys	Ser	Thr	Arg	Cys	Gly	Tyr	Cys	Asp	
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ttc	aac	acc	tat	act	gct	ggg	gaa	tta	ggg	agt	act	gca	ggc	ccg	gac	211
Phe	Asn	Thr	Tyr	Thr	Ala	Gly	Glu	Leu	Gly	Ser	Thr	Ala	Gly	Pro	Asp	
			25					30					35			
acc	tat	ctt	gac	tcg	ttg	gaa	gtt	gag	ttg	gag	atg	gct	gtg	gct	tcg	259
Thr	Tyr	Leu	Asp	Ser	Leu	Glu	Val	Glu	Leu	Glu	Met	Ala	Val	Ala	Ser	
		40				45						50				
ctg	gat	aat	cct	cgg	cag	gcg	gaa	act	atc	ttt	att	ggc	ggg	ggg	acc	307
Leu	Asp	Asn	Pro	Arg	Gln	Ala	Glu	Thr	Ile	Phe	Ile	Gly	Gly	Gly	Thr	
	55					60					65					
ccg	tcg	ttg	att	ggg	gcg	gac	ggg	ttg	gcc	agg	gtt	ttg	ggg	gct	gtg	355
Pro	Ser	Leu	Ile	Gly	Ala	Asp	Gly	Leu	Ala	Arg	Val	Leu	Gly	Ala	Val	
70					75				80						85	
cgc	aat	act	ttt	ggc	att	gcg	gat	ggg	gcg	gaa	gtc	acc	acg	gag	tcc	403
Arg	Asn	Thr	Phe	Gly	Ile	Ala	Asp	Gly	Ala	Glu	Val	Thr	Thr	Glu	Ser	
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aat	ccg	gag	tct	acc	tcg	cct	gag	ttt	ttt	gat	ggc	ctg	cgt	gag	gcg	451
Asn	Pro	Glu	Ser	Thr	Ser	Pro	Glu	Phe	Phe	Asp	Gly	Leu	Arg	Glu	Ala	
			105					110					115			
ggc	tac	aac	agg	att	tcg	tta	ggg	atg	cag	tcg	gcg	tcg	tca	agc	gtt	499
Gly	Tyr	Asn	Arg	Ile	Ser	Leu	Gly	Met	Gln	Ser	Ala	Ser	Ser	Ser	Val	
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Leu	Lys	Val	Leu	Asp	Arg	Thr	His	Thr	Pro	Gly	Arg	Pro	Val	Ala	Ala	
	135					140					145					
gcc	aag	gag	gca	cgt	gag	gcg	ggg	ttt	gag	cat	gtc	aat	ttg	gac	atg	595
Ala	Lys	Glu	Ala	Arg	Glu	Ala	Gly	Phe	Glu	His	Val	Asn	Leu	Asp	Met	
150					155					160					165	
att	tat	ggc	acg	ccg	aca	gag	acc	gat	gat	gat	gtc	cgc	aag	acg	ctg	643
Ile	Tyr	Gly	Thr	Pro	Thr	Glu	Thr	Asp	Asp	Asp	Val	Arg	Lys	Thr	Leu	
				170					175					180		
aat	gcg	gtg	ctc	gaa	gcg	aac	gtg	gat	cac	gtg	tct	gcc	tat	tcc	ttg	691
Asn	Ala	Val	Leu	Glu	Ala	Asn	Val	Asp	His	Val	Ser	Ala	Tyr	Ser	Leu	
			185					190					195			
atc	gtg	aaa	gat	ggc	acg	gcg	atg	gcg	cgc	aag	gtg	cac	aag	ggc	gag	739
Ile	Val	Lys	Asp	Gly	Thr	Ala	Met	Ala	Arg	Lys	Val	His	Lys	Gly	Glu	
		200				205						210				
ctg	cca	gcg	ccg	gac	gag	gat	gtc	tac	gct	gat	cgt	ttt	gag	ctt	atc	787
Leu	Pro	Ala	Pro	Asp	Glu	Asp	Val	Tyr	Ala	Asp	Arg	Phe	Glu	Leu	Ile	
	215					220					225					
gac	gct	cgc	ctg	cgc	tca	gct	ggg	ttc	gat	tgg	tac	gag	gtg	tcc	aac	835
Asp	Ala	Arg	Leu	Arg	Ser	Ala	Gly	Phe	Asp	Trp	Tyr	Glu	Val	Ser	Asn	
230					235				240						245	
tgg	gcg	aaa	ccc	ggc	gga	gaa	tgc	aag	cac	aac	atg	ggc	tat	tgg	gtc	883
Trp	Ala	Lys	Pro	Gly	Gly	Glu	Cys	Lys	His	Asn	Met	Gly	Tyr	Trp	Val	

250										255					260					
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265 270 275																				
gac cgc cgc ttc tac aac atc aag cac cca gcg cgt tac tcc gcg cag	979																			
Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala Arg Tyr Ser Ala Gln																				
280 285 290																				
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Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr Glu Arg Leu Thr Ala																				
295 300 305																				
gaa gat cac cac acc gag cgc gtc atg ctt ggt ttg cgc ctg aaa caa	1075																			
Glu Asp His His Thr Glu Arg Val Met Leu Gly Leu Arg Leu Lys Gln																				
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Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala Arg Pro Val Ile Asp																				
330 335 340																				
cgt cat atc gca ggg ggc ctg ctg cac gtc aat gcg ctg ggc aac ctg	1171																			
Arg His Ile Ala Gly Gly Leu Leu His Val Asn Ala Leu Gly Asn Leu																				
345 350 355																				
gcg gtg acc gat gcg gga cgt ttg ctt gcc gac ggc atc atc gcc gac	1219																			
Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp Gly Ile Ile Ala Asp																				
360 365 370																				
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<210> 802

<211> 380

<212> PRT

<213> Corynebacterium glutamicum

<400> 802

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Thr Ala Gly Pro Asp Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu
35 40 45

Met Ala Val Ala Ser Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe
50 55 60

Ile Gly Gly Gly Thr Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg
65 70 75 80

Val Leu Gly Ala Val Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu
85 90 95

Val Thr Thr Glu Ser Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp
100 105 110

Gly Leu Arg Glu Ala Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser
 115 120 125
 Ala Ser Ser Ser Val Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly
 130 135 140
 Arg Pro Val Ala Ala Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His
 145 150 155 160
 Val Asn Leu Asp Met Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp
 165 170 175
 Val Arg Lys Thr Leu Asn Ala Val Leu Glu Ala Asn Val Asp His Val
 180 185 190
 Ser Ala Tyr Ser Leu Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys
 195 200 205
 Val His Lys Gly Glu Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp
 210 215 220
 Arg Phe Glu Leu Ile Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp
 225 230 235 240
 Tyr Glu Val Ser Asn Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn
 245 250 255
 Met Gly Tyr Trp Val Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala
 260 265 270
 His Ser His Ile Gly Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala
 275 280 285
 Arg Tyr Ser Ala Gln Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr
 290 295 300
 Glu Arg Leu Thr Ala Glu Asp His His Thr Glu Arg Val Met Leu Gly
 305 310 315 320
 Leu Arg Leu Lys Gln Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala
 325 330 335
 Arg Pro Val Ile Asp Arg His Ile Ala Gly Gly Leu Leu His Val Asn
 340 345 350
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 355 360 365
 Gly Ile Ile Ala Asp Ile Leu Leu Ser Glu Glu Asp
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<210> 803

<211> 522

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(499)

<223> RXN02503

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ttcgtgaacg caccttctgc cacacaaacg agggagtaac atg acc tta aaa att 115
Met Thr Leu Lys Ile
1 5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163
Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg
10 15 20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211
Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr
25 30 35

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
40 45 50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
55 60 65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
70 75 80 85

ttc cac ctg gtc gtg cca act cgt gcg gac tcg cgc gag gcc ctt atc 403
Phe His Leu Val Val Pro Thr Arg Ala Asp Ser Arg Glu Ala Leu Ile
90 95 100

gcc cgc gac ggc ctg act ctg gct gag ctt cca gaa agg cgc aaa ggt 451
Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro Glu Arg Arg Lys Gly
105 110 115

ggg aac ttc cgc tcc tcg acg cat ctc cca gct caa ggc aat ccg ccc 499
Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala Gln Gly Asn Pro Pro
120 125 130

tgacctggag attctccac tgc 522

<210> 804

<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 804

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Ala Gly Thr Ile Arg Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu
20 25 30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu
35 40 45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His
50 55 60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr
 65 70 75 80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Ser
 85 90 95

Arg Glu Ala Leu Ile Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro
 100 105 110

Glu Arg Arg Lys Gly Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala
 115 120 125

Gln Gly Asn Pro Pro
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<210> 805

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(535)

<223> FRXA02503

<400> 805

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 Met Thr Leu Lys Ile
 1 5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163
 Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg
 10 15 20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211
 Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr
 25 30 35

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
 Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
 40 45 50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
 Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
 55 60 65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
 Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
 70 75 80 85

ttc cac ctg gtc gtg cca act cgt gcg gac tck cgc cga ggs cct tat 403
 Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa Arg Arg Xaa Pro Tyr
 90 95 100

cgc ccn cga cgg sct gan ttt kgg ttr agc tty caa aar gsg saa agg 451
 Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa Gln Xaa Xaa Xaa Arg
 105 110 115

tgg gaa ctt tcc gct cct cga cgc atc tcc cag ctc aag gca atc cgc 499
 Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
 120 125 130

cct gac ctg gag att ctc cca ctt gcg cgg aaa cat tgacaccggc 545
 Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys His
 135 140 145

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<210> 806

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 806

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 20 25 30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu
 35 40 45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His
 50 55 60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr
 65 70 75 80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa
 85 90 95

Arg Arg Xaa Pro Tyr Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa
 100 105 110

Gln Xaa Xaa Xaa Arg Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln
 115 120 125

Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys
 130 135 140

His

145

<210> 807

<211> 1245

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1222)

<223> RXA00377

<400> 807

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				Val	Trp	Leu	Leu	Phe	
				1				5	
cta aat tgg gat aaa tgg ggc aag att gag cgc atg tct gct ctt act	163								
Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg Met Ser Ala Leu Thr									
	10 15 20								
att cca gct gcg cgt cgc acg cta aat aac gcg ccc att att gat gcc	211								
Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala Pro Ile Ile Asp Ala									
	25 30 35								
gct aat ggc aag acc ccg act cgc act ccg gtg tgg ttt atg cgc cag	259								
Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val Trp Phe Met Arg Gln									
	40 45 50								
gcg ggt agg tcg ttg cct gag tac aag aag gtc cgt gag gga atc agc	307								
Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val Arg Glu Gly Ile Ser									
	55 60 65								
atg ttg gat tcc tgt ttc atg ccg gag ttg ttg gcg gag att act ttg	355								
Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu Ala Glu Ile Thr Leu									
	70 75 80 85								
cag ccg gtt cgt cgt cat gat gtg gat gct gcg att ttg ttc tct gac	403								
Gln Pro Val Arg Arg His Asp Val Asp Ala Ala Ile Leu Phe Ser Asp									
	90 95 100								
att gtg gtg ccg ttg cgt gct gcg ggt gtt ggt gtg gaa atc gtg gcg	451								
Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly Val Glu Ile Val Ala									
	105 110 115								
ggt cgt gga cct gtg ttg gat gcg ccg gtg cgg agc cgt ggg gat gtg	499								
Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg Ser Arg Gly Asp Val									
	120 125 130								
ttg aat ctt cct att ttg gag ggc aac gtt ccg gag gtg gag cag ggt	547								
Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro Glu Val Glu Gln Gly									
	135 140 145								
att ggc atc att ttg gat gag ttg tct gat tct cag gcg ttg att ggt	595								
Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser Gln Ala Leu Ile Gly									
	150 155 160 165								
ttt gct ggt gcg ccg ttt acg ttg gcg agt tac ttg gtt gag ggt ggt	643								
Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr Leu Val Glu Gly Gly									
	170 175 180								
cct tcc aag aat cat gag aag acc aaa gca atg atg cat ggt gat cct	691								
Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met Met His Gly Asp Pro									
	185 190 195								
gag acg tgg cat gcg ttg atg gct cgt ttg gtg ccg acg att gtg aat	739								
Glu Thr Trp His Ala Leu Met Ala Arg Leu Val Pro Thr Ile Val Asn									
	200 205 210								
tct ttg aag tcg cag atc gat gcg ggt atc gat gcg gtg cag ttg ttt	787								
Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp Ala Val Gln Leu Phe									
	215 220 225								

gat	tcg	tgg	gct	ggg	ttc	ctc	act	gag	cgt	gat	tac	acc	gag	ttc	gtg	835
Asp	Ser	Trp	Ala	Gly	Phe	Leu	Thr	Glu	Arg	Asp	Tyr	Thr	Glu	Phe	Val	
230					235					240					245	
ttg	ccg	tat	tcc	act	gag	att	ttg	gag	gaa	gtg	ggc	aag	tac	cag	ctg	883
Leu	Pro	Tyr	Ser	Thr	Glu	Ile	Leu	Glu	Glu	Val	Gly	Lys	Tyr	Gln	Leu	
				250					255					260		
cct	cgt	att	cac	ttt	ggg	gtg	ggg	act	ggg	gag	ttg	ctt	ggg	gcg	atg	931
Pro	Arg	Ile	His	Phe	Gly	Val	Gly	Thr	Gly	Glu	Leu	Leu	Gly	Ala	Met	
			265					270						275		
agc	aag	gct	ggc	tca	gag	gtc	atg	ggg	gtg	gat	tgg	cgg	gtg	ccg	ttg	979
Ser	Lys	Ala	Gly	Ser	Glu	Val	Met	Gly	Val	Asp	Trp	Arg	Val	Pro	Leu	
		280					285					290				
gat	aag	gct	gcg	gag	cgt	att	gct	gcg	gta	tca	ggg	cct	aag	gtg	ttg	1027
Asp	Lys	Ala	Ala	Glu	Arg	Ile	Ala	Ala	Val	Ser	Gly	Pro	Lys	Val	Leu	
	295					300					305					
cag	ggg	aac	ctc	gat	cct	gcg	ttg	ttg	ttt	gcg	ggg	cgc	gca	cct	ttg	1075
Gln	Gly	Asn	Leu	Asp	Pro	Ala	Leu	Leu	Phe	Ala	Gly	Arg	Ala	Pro	Leu	
310					315					320					325	
act	aag	gaa	att	gag	cgc	atc	aag	gca	gag	gct	cag	act	gct	gtt	gat	1123
Thr	Lys	Glu	Ile	Glu	Arg	Ile	Lys	Ala	Glu	Ala	Gln	Thr	Ala	Val	Asp	
				330					335					340		
gca	ggg	cat	gca	acg	ggc	cat	atc	ttt	aac	ctt	ggg	cat	ggg	gtg	ctt	1171
Ala	Gly	His	Ala	Thr	Gly	His	Ile	Phe	Asn	Leu	Gly	His	Gly	Val	Leu	
			345					350					355			
cct	aat	acg	gtg	gcg	gaa	gat	att	act	gaa	gcc	gtc	tcc	atc	att	cat	1219
Pro	Asn	Thr	Val	Ala	Glu	Asp	Ile	Thr	Glu	Ala	Val	Ser	Ile	Ile	His	
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tct	taa	act	aaga	ggag	ttt	cat	gcg									1245
Ser																

<210> 808

<211> 374

<212> PRT

<213> Corynebacterium glutamicum

<400> 808

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			20					25					30			
Pro	Ile	Ile	Asp	Ala	Ala	Asn	Gly	Lys	Thr	Pro	Thr	Arg	Thr	Pro	Val	
		35					40					45				
Trp	Phe	Met	Arg	Gln	Ala	Gly	Arg	Ser	Leu	Pro	Glu	Tyr	Lys	Lys	Val	
	50					55					60					
Arg	Glu	Gly	Ile	Ser	Met	Leu	Asp	Ser	Cys	Phe	Met	Pro	Glu	Leu	Leu	
65					70					75					80	

Ala Glu Ile Thr Leu Gln Pro Val Arg Arg His Asp Val Asp Ala Ala
 85 90 95
 Ile Leu Phe Ser Asp Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly
 100 105 110
 Val Glu Ile Val Ala Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg
 115 120 125
 Ser Arg Gly Asp Val Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro
 130 135 140
 Glu Val Glu Gln Gly Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser
 145 150 155 160
 Gln Ala Leu Ile Gly Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr
 165 170 175
 Leu Val Glu Gly Gly Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met
 180 185 190
 Met His Gly Asp Pro Glu Thr Trp His Ala Leu Met Ala Arg Leu Val
 195 200 205
 Pro Thr Ile Val Asn Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp
 210 215 220
 Ala Val Gln Leu Phe Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp
 225 230 235 240
 Tyr Thr Glu Phe Val Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val
 245 250 255
 Gly Lys Tyr Gln Leu Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu
 260 265 270
 Leu Leu Gly Ala Met Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp
 275 280 285
 Trp Arg Val Pro Leu Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser
 290 295 300
 Gly Pro Lys Val Leu Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala
 305 310 315 320
 Gly Arg Ala Pro Leu Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala
 325 330 335
 Gln Thr Ala Val Asp Ala Gly His Ala Thr Gly His Ile Phe Asn Leu
 340 345 350
 Gly His Gly Val Leu Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala
 355 360 365
 Val Ser Ile Ile His Ser
 370

<210> 809

<211> 681

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(658)

<223> RXN02504

<400> 809

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gacggcctga ctctggctga gcttccagaa aggcgcaaag gtg gga act tcc gct 115
                               Val Gly Thr Ser Ala
                               1         5

cct cga cgc atc tcc cag ctc aag gca atc cgc cct gac ctg gag att 163
Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile
                10                15                20

ctc cca ctg cgc gga aac att gac acc ggc atg ggc aag gtc acc tcc 211
Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met Gly Lys Val Thr Ser
                25                30                35

ggg gaa ctc gat gct gtg atg ctc gcc tac gca ggc ctc acc cgc gtc 259
Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala Gly Leu Thr Arg Val
                40                45                50

ggc atg cag gac cgc gca acg gaa gtt ttc gac gcc gac atc atc atg 307
Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met
                55                60                65

ccc gcc ccc gca cag ggc gca ctt gcg atc gaa tgc cgc gcc gac gac 355
Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp
                70                75                80                85

act gaa acc gtc cgc gcg ctc aac atg ctg atg cac gcc gac acg ttt 403
Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe
                90                95                100

gtt tcc gcg gtt gca gaa cgc acc gtg ctc aac cgc ctc gaa gct ggc 451
Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly
                105                110                115

tgt acc gcg cct gtc gca gcg cac gcc acc ttg gac ggc tac tcc ggc 499
Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly
                120                125                130

gac acc atg act ctc acc gcc ggc gtc tac gca ctt gac ggc tct gac 547
Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp
                135                140                145

cag ctg gta ttc tcc gcc gaa ggt gac ggc gcc cgc cca gaa gag ctc 595
Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu
                150                155                160                165

ggc gag ctc gtt gca caa cag ctt atc gac gcc gga gcc gcc aat ttg 643
Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu
                170                175                180

ctc ggc gac cgc agc taattagggc ccgaaatttc cat 681
Leu Gly Asp Arg Ser

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185

<210> 810

<211> 186

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 810

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 20 25 30

Gly Lys Val Thr Ser Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala
 35 40 45

Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp
 50 55 60

Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu
 65 70 75 80

Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met
 85 90 95

His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn
 100 105 110

Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu
 115 120 125

Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala
 130 135 140

Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala
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Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala
 165 170 175

Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser
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<210> 811

<211> 561

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(538)

<223> FRXA02504

<400> 811

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 Met Leu Val Met Leu

	1	5	
gcc tac gca ggc ctc acc cgc gtc ggc atg cag gac cgc gca acg gaa			163
Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu			
	10	20	
ggt ttc gac gcc gac atc atc atg ccc gcc ccc gca cag ggc gca ctt			211
Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu			
	25	35	
gcg atc gaa tgc cgc gcc gac gac act gaa acc gtc cgc gcg ctc aac			259
Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn			
	40	50	
atg ctg atg cac gcc gac acg ttt gtt tcc gcg gtt gca gaa cgc acc			307
Met Leu Met His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr			
	55	65	
gtg ctc aac cgc ctc gaa gct ggc tgt acc gcg cct gtc gca gcg cac			355
Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His			
	70	85	
gcc acc ttg gac ggc tac tcc ggc gac acc atg act ctc acc gcc ggc			403
Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly			
	90	100	
gtc tac gca ctt gac ggc tct gac cag ctg gta ttc tcc gcc gaa ggt			451
Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly			
	105	115	
gac ggc gcc cgc cca gaa gag ctc ggc gag ctc gtt gca caa cag ctt			499
Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu			
	120	130	
atc gac gcc gga gcc gcc aat ttg ctc ggc gac cgc agc taattagggc			548
Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser			
	135	145	
ccgaaatttc cat			561

<210> 812

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 812

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Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro			
	20	25	30
Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr			
	35	40	45
Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe Val Ser Ala			
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Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala			
	65	70	75
			80

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<210> 813
<211> 1449
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (1426)
<223> RXN01162
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<400> 813																																
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								Met		Tyr		Ile		Val		Gly		5														
att		tgt		cta		caa		tta		gtg		gtt		atg		agc		caa		ccg		atg		tca		gca		ccc		gac		163
Ile		Cys		Leu		Gln		Leu		Val		Val		Met		Ser		Gln		Pro		Met		Ser		Ala		Pro		Asp		
								10										15										20				
tcc		gct		cca		gga		aca		gag		cgc		ggc		cat		gaa		cgc		acc		cat		ttt		gcg		gta		211
Ser		Ala		Pro		Gly		Thr		Glu		Arg		Gly		His		Glu		Arg		Thr		His		Phe		Ala		Val		
						25										30										35						
gtc		ggc		gac		tcc		cag		gat		cca		gca		cag		gca		aca		gct		cct		aga		gcg		cca		259
Val		Gly		Asp		Ser		Gln		Asp		Pro		Ala		Gln		Ala		Thr		Ala		Pro		Arg		Ala		Pro		
				40								45										50										
gca		gaa		tca		att		act		ttg		att		ggc		att		ggc		acc		gat		ggg		ttt		gag		ggg		307
Ala		Glu		Ser		Ile		Thr		Leu		Ile		Gly		Ile		Gly		Thr		Asp		Gly		Phe		Glu		Gly		
		55								60										65												
ctc		gga		ctc		aag		gca		cag		caa		gca		tta		caa		cgt		gcc		tct		gtg		gtg		att		355
Leu		Gly		Leu		Lys		Ala		Gln		Gln		Ala		Leu		Gln		Arg		Ala		Ser		Val		Val		Ile		
70										75								80												85		
gga		tca		tgg		cgc		cag		ctc		aat		ctc		gta		cct		gat		gcc		att		aag		gca		gag		403
Gly		Ser		Trp		Arg		Gln		Leu		Asn		Leu		Val		Pro		Asp		Ala		Ile		Lys		Ala		Glu		
								90								95										100						
cgt		cgc		cca		tgg		ccg		ggc		aat		acc		aag		cat		cct		gat		tta		gat		gcc		ttg		451
Arg		Arg		Pro		Trp		Pro		Gly		Asn		Thr		Lys		His		Pro		Asp		Leu		Asp		Ala		Leu		
				105										110										115								

ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat	499
Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp	
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cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg	547
Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met	
135 140 145	
gat aga ctc acg gtt att ccg gga cca tca tcc gcg tcg ctt gct tgc	595
Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys	
150 155 160 165	
gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga	643
Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly	
170 175 180	
caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa	691
Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln	
185 190 195	
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Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr	
200 205 210	
ttg ttg aat gaa ctc gga ctg ggg gag act cca ctg act gtg ctc agc	787
Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser	
215 220 225	
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat	835
Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His	
230 235 240 245	
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc	883
Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg	
250 255 260	
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac	931
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp	
265 270 275	
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg	979
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met	
280 285 290	
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta	1027
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu	
295 300 305	
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt	1075
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val	
310 315 320 325	
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt	1123
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser	
330 335 340	
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta	1171
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val	
345 350 355	

caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc 1219
 Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly
 360 365 370

cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct 1267
 Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro
 375 380 385

gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag 1315
 Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys
 390 395 400 405

ctt cac aca ctc caa gaa caa cac ggc gga atc atc aaa cac atc cgc 1363
 Leu His Thr Leu Gln Glu Gln His Gly Gly Ile Ile Lys His Ile Arg
 410 415 420

atc gac gac aca gac gtg cac caa tgg cga gtt aca aag ccg gtg act 1411
 Ile Asp Asp Thr Asp Val His Gln Trp Arg Val Thr Lys Pro Val Thr
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cca gaa gcg gtg aat tagcatcaaaa aaccaacccc atg 1449
 Pro Glu Ala Val Asn
 440

<210> 814

<211> 442

<212> PRT

<213> Corynebacterium glutamicum

<400> 814

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 20 25 30

Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
 35 40 45

Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
 50 55 60

Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
 65 70 75 80

Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
 85 90 95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro
 100 105 110

Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val
 115 120 125

Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val
 130 135 140

His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser
 145 150 155 160

Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg
 165 170 175
 Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile
 180 185 190
 Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr
 195 200 205
 Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro
 210 215 220
 Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln
 225 230 235 240
 Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile
 245 250 255
 Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp
 260 265 270
 Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro
 275 280 285
 Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu
 290 295 300
 Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser
 305 310 315 320
 Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly
 325 330 335
 Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys
 340 345 350
 Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile
 355 360 365
 Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp
 370 375 380
 Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu
 385 390 395 400
 Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly Ile
 405 410 415
 Ile Lys His Ile Arg Ile Asp Asp Thr Asp Val His Gln Trp Arg Val
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 Thr Lys Pro Val Thr Pro Glu Ala Val Asn
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<210> 815

<211> 1345

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1345)

<223> FRXA01162

<400> 815

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Met Tyr Ile Val Gly
1 5

att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163
Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro Met Ser Ala Pro Asp
10 15 20

tcc gct cca gga aca gag cgc ggt cat gaa cgc acc cat ttt gcg gta 211
Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg Thr His Phe Ala Val
25 30 35

gtc ggt gac tcc cag gat cca gca cag gca aca gct cct aga gcg cca 259
Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr Ala Pro Arg Ala Pro
40 45 50

gca gaa tca att act ttg att ggt att ggt acc gat ggg ttt gag ggg 307
Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr Asp Gly Phe Glu Gly
55 60 65

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Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg Ala Ser Val Val Ile
70 75 80 85

gga tca tgg cgc cag ctc aat ctc gta cct gat gcc att aag gca gag 403
Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp Ala Ile Lys Ala Glu
90 95 100

cgt cgc cca tgg ccg ggt aat acc aag cat cct gat tta gat gcc ttg 451
Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro Asp Leu Asp Ala Leu
105 110 115

ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat 499
Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp
120 125 130

cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg 547
Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met
135 140 145

gat aga ctc acg gtt att ccg gga cca tca tcc gcg tcg ctt gct tgc 595
Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys
150 155 160 165

gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga 643
Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly
170 175 180

caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa 691
Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln
185 190 195

ttc ctc gtc ttg ggt aaa gat gaa ttc agt aca gct caa gtt gcc acg 739
Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr

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200	205	210	
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Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser			
215	220	225	
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat			835
Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His			
230	235	240	245
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc			883
Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg			
	250	255	260
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac			931
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp			
	265	270	275
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg			979
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met			
	280	285	290
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta			1027
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu			
	295	300	305
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt			1075
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val			
	310	315	320
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt			1123
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser			
	330	335	340
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta			1171
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val			
	345	350	355
caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc			1219
Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly			
	360	365	370
cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct			1267
Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro			
	375	380	385
gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag			1315
Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys			
	390	395	400
ctt cac aca ctc caa gaa caa cac ggc gga			1345
Leu His Thr Leu Gln Glu Gln His Gly Gly			
	410	415	

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<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 816

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Met	Ser	Ala	Pro	Asp	Ser	Ala	Pro	Gly	Thr	Glu	Arg	Gly	His	Glu	Arg	20	25	30	
Thr	His	Phe	Ala	Val	Val	Gly	Asp	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Thr	35	40	45	
Ala	Pro	Arg	Ala	Pro	Ala	Glu	Ser	Ile	Thr	Leu	Ile	Gly	Ile	Gly	Thr	50	55	60	
Asp	Gly	Phe	Glu	Gly	Leu	Gly	Leu	Lys	Ala	Gln	Gln	Ala	Leu	Gln	Arg	65	70	75	80
Ala	Ser	Val	Val	Ile	Gly	Ser	Trp	Arg	Gln	Leu	Asn	Leu	Val	Pro	Asp	85	90	95	
Ala	Ile	Lys	Ala	Glu	Arg	Arg	Pro	Trp	Pro	Gly	Asn	Thr	Lys	His	Pro	100	105	110	
Asp	Leu	Asp	Ala	Leu	Phe	Lys	Glu	Phe	Leu	Gly	Arg	His	Val	Ala	Val	115	120	125	
Leu	Ala	Ser	Gly	Asp	Pro	Leu	Phe	Tyr	Gly	Val	Gly	Thr	Ala	Met	Val	130	135	140	
His	Val	Leu	Gly	Met	Asp	Arg	Leu	Thr	Val	Ile	Pro	Gly	Pro	Ser	Ser	145	150	155	160
Ala	Ser	Leu	Ala	Cys	Ala	Arg	Leu	Gly	Trp	Thr	Val	Asn	Arg	Thr	Arg	165	170	175	
Val	Val	Tyr	Leu	Gly	Gln	Glu	Pro	Ile	Glu	Thr	Leu	Ile	Pro	Ile	Ile	180	185	190	
Glu	Ser	Gly	Ala	Gln	Phe	Leu	Val	Leu	Gly	Lys	Asp	Glu	Phe	Ser	Thr	195	200	205	
Ala	Gln	Val	Ala	Thr	Leu	Leu	Asn	Glu	Leu	Gly	Leu	Gly	Glu	Thr	Pro	210	215	220	
Leu	Thr	Val	Leu	Ser	Asp	Leu	Gly	Ser	Thr	Asp	Glu	Glu	Ile	Thr	Gln	225	230	235	240
Gly	Thr	Ala	Ser	His	Pro	Pro	Ala	Ala	Val	Ser	Val	Leu	Asn	Val	Ile	245	250	255	
Ala	Val	Gly	Ala	Arg	Thr	Ala	Met	Pro	Lys	Pro	His	Phe	Glu	Gly	Asp	260	265	270	
Val	Ser	Asn	Glu	Asp	Leu	Arg	Ala	Leu	Thr	Val	Ala	Ala	Leu	Glu	Pro	275	280	285	
Thr	Gln	Gly	Gln	Met	Leu	Trp	Thr	Phe	Gly	Asp	Ile	Gly	Ala	Ala	Leu	290	295	300	
Ala	Cys	Asp	Trp	Leu	Arg	Ala	Ala	Gly	Asn	Lys	Ala	His	Ala	Ile	Ser	305	310	315	320
Phe	Ala	Ser	Met	Val	Glu	Gln	Ser	Gln	Arg	Asn	Ala	Arg	Lys	Leu	Gly				

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Val	Ser	Thr	Leu	Ser	Val	Lys	Glu	Thr	Leu	Ser	Pro	Lys	Thr	Leu	Lys				
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Asp	Ile	Arg	Tyr	Val	Gln	Gly	Pro	Glu	Ser	Ala	Ser	Pro	His	Ala	Ile				
		355					360					365							
Phe	Met	Asn	Lys	Gly	Leu	Gly	Ile	Asp	Leu	Val	Pro	Glu	Thr	Ala	Trp				
	370					375					380								
Met	Met	Leu	Arg	Pro	Gly	Gly	Lys	Leu	Ile	Ala	Gln	Ala	Ser	Thr	Glu				
385					390					395					400				
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<213> Corynebacterium glutamicum

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<223> RXA01692

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gaa	aac	cag	cca	ata	atc	cag	cca	gtc	tcc	tta	att	ggg	gga	ggg	cct	163
Glu	Asn	Gln	Pro	Ile	Ile	Gln	Pro	Val	Ser	Leu	Ile	Gly	Gly	Gly	Pro	
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ggg	gca	tgg	gac	tta	att	acg	gtg	cgt	ggg	atg	aat	cgc	ctt	cag	gag	211
Gly	Ala	Trp	Asp	Leu	Ile	Thr	Val	Arg	Gly	Met	Asn	Arg	Leu	Gln	Glu	
			25					30					35			

gct	gat	gtc	att	ttg	gct	gat	cac	ttg	ggg	ccc	act	gat	gag	ttg	gaa	259
Ala	Asp	Val	Ile	Leu	Ala	Asp	His	Leu	Gly	Pro	Thr	Asp	Glu	Leu	Glu	
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aaa	ttg	tgc	gac	atc	agc	tcg	aag	act	gtt	gtt	gat	gtg	tcc	aag	ctt	307
Lys	Leu	Cys	Asp	Ile	Ser	Ser	Lys	Thr	Val	Val	Asp	Val	Ser	Lys	Leu	
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ccg	tat	ggg	cgg	cag	gtc	act	cag	gag	cgt	act	aat	gag	atg	ctt	gtt	355
Pro	Tyr	Gly	Arg	Gln	Val	Thr	Gln	Glu	Arg	Thr	Asn	Glu	Met	Leu	Val	
	70				75				80					85		

gaa	tac	gca	cag	cag	gga	cta	aag	gtg	gtt	cgc	ctt	aaa	ggg	ggg	gac	403
Glu	Tyr	Ala	Gln	Gln	Gly	Leu	Lys	Val	Val	Arg	Leu	Lys	Gly	Gly	Asp	
			90					95						100		

cct	tat	gtc	ttc	ggg	cgg	ggg	ttt	gaa	gag	ttg	gag	ttt	ttg	ggc	gag	451
Pro	Tyr	Val	Phe	Gly	Arg	Gly	Phe	Glu	Glu	Leu	Glu	Phe	Leu	Gly	Glu	

105					110					115						
cat	gga	att	gaa	tgc	gag	gtc	att	ccg	ggt	gtg	acc	agt	gcg	gtg	tcc	499
His	Gly	Ile	Glu	Cys	Glu	Val	Ile	Pro	Gly	Val	Thr	Ser	Ala	Val	Ser	
	120						125					130				
ggt	cca	gcg	gcg	gca	ggt	att	cct	att	act	aat	cgg	gga	gtg	gtg	cat	547
Val	Pro	Ala	Ala	Ala	Gly	Ile	Pro	Ile	Thr	Asn	Arg	Gly	Val	Val	His	
	135					140					145					
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Ser	Phe	Thr	Val	Val	Ser	Gly	His	Leu	Pro	Pro	Gly	His	Pro	Lys	Ser	
150					155					160					165	
ctg	gtt	gat	tgg	gct	gcg	ttg	gcc	aaa	tcg	ggt	ggc	acc	ttg	tcc	atc	643
Leu	Val	Asp	Trp	Ala	Ala	Leu	Ala	Lys	Ser	Gly	Gly	Thr	Leu	Ser	Ile	
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atc	atg	ggt	gtg	aaa	aat	gcg	ggt	gcg	att	gcc	cag	gcg	ctc	atg	gac	691
Ile	Met	Gly	Val	Lys	Asn	Ala	Gly	Ala	Ile	Ala	Gln	Ala	Leu	Met	Asp	
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ggc	ggg	ctt	gat	gca	gat	act	cca	gca	gct	gtt	att	cag	gaa	ggc	act	739
Gly	Gly	Leu	Asp	Ala	Asp	Thr	Pro	Ala	Ala	Val	Ile	Gln	Glu	Gly	Thr	
		200					205					210				
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Thr	Asp	Ala	Gln	Arg	Ser	Val	Arg	Cys	Thr	Leu	Gly	Thr	Leu	Gly	Ala	
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Val	Met	Val	Glu	Glu	Glu	Ile	Lys	Pro	Pro	Ala	Val	Tyr	Val	Ile	Gly	
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<213> Corynebacterium glutamicum

<400> 818

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15

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20

25

30

Asn Arg Leu Gln Glu Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro

35

40

45

Thr Asp Glu Leu Glu Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val

50

55

60

Asp Val Ser Lys Leu Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr

65

70

75

80

Asn Glu Met Leu Val Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg

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Leu	Lys	Gly	Gly	Asp	Pro	Tyr	Val	Phe	Gly	Arg	Gly	Phe	Glu	Glu	Leu
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Glu	Phe	Leu	Gly	Glu	His	Gly	Ile	Glu	Cys	Glu	Val	Ile	Pro	Gly	Val
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Thr	Ser	Ala	Val	Ser	Val	Pro	Ala	Ala	Ala	Gly	Ile	Pro	Ile	Thr	Asn
130								135				140			
Arg	Gly	Val	Val	His	Ser	Phe	Thr	Val	Val	Ser	Gly	His	Leu	Pro	Pro
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Gly	His	Pro	Lys	Ser	Leu	Val	Asp	Trp	Ala	Ala	Leu	Ala	Lys	Ser	Gly
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Gly	Thr	Leu	Ser	Ile	Ile	Met	Gly	Val	Lys	Asn	Ala	Gly	Ala	Ile	Ala
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Gln	Ala	Leu	Met	Asp	Gly	Gly	Leu	Asp	Ala	Asp	Thr	Pro	Ala	Ala	Val
195								200				205			
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210								215				220			
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Met Thr Ile Ala His																
1 5																
aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc																163
Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser																
10 15 20																
gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt																211
Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val																
25 30 35																
tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca																259
Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro																
40 45 50																

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Gly	Lys	Val	Ile	Phe	Val	Gly	Ala	Gly	Pro	Gly	Asn	Pro	Asp	Leu	Leu	
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Thr	Val	Arg	Ala	Arg	Glu	Val	Leu	Gly	Asn	Ala	Val	Arg	Ala	Ile	Thr	
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Asp	Glu	Gln	Val	Leu	Ser	Gly	Val	Arg	Ala	Phe	Val	Ala	Thr	Glu	Ile	
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cct	gtg	ccg	gaa	gat	aag	ctt	cag	gct	gcg	gaa	gat	gag	tac	gag	cgc	451
Pro	Val	Pro	Glu	Asp	Lys	Leu	Gln	Ala	Ala	Glu	Asp	Glu	Tyr	Glu	Arg	
			105				110						115			
atc	tgc	att	gaa	gcg	aag	gag	aac	ggg	gca	cgc	cgt	aag	cct	cct	cgt	499
Ile	Cys	Ile	Glu	Ala	Lys	Glu	Asn	Gly	Ala	Arg	Arg	Lys	Pro	Pro	Arg	
	120						125					130				
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Pro	Ala	Pro	Pro	Thr	Ala	Ala	Glu	Ile	Thr	Glu	Val	Ser	Glu	Ala	Thr	
	135					140					145					
cca	gct	cag	att	gtt	gag	ctt	gtg	cag	gat	gct	ctt	tct	tat	ggg	gga	595
Pro	Ala	Gln	Ile	Val	Glu	Leu	Val	Gln	Asp	Ala	Leu	Ser	Tyr	Gly	Gly	
	150				155				160					165		
gat	gtt	att	cgt	ctt	gtc	acc	ggc	aac	cca	ttg	agc	agc	gat	gcc	aca	643
Asp	Val	Ile	Arg	Leu	Val	Thr	Gly	Asn	Pro	Leu	Ser	Ser	Asp	Ala	Thr	
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Leu	Ala	Glu	Ile	Ser	Ala	Val	Ser	Glu	Ala	Gly	Leu	Glu	Phe	Gln	Val	
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Val	Pro	Gly	Met	Ser	Leu	Pro	Ala	Thr	Val	Pro	Ala	Phe	Ala	Gly	Ile	
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Ala	Leu	Gly	Ser	Thr	Tyr	Thr	Glu	Thr	Asp	Val	Asn	Gly	Gln	Asn	Leu	
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gac	tgg	gat	cag	ttg	gct	agc	gca	cct	cag	cct	ttg	gtg	ctg	cag	gcc	835
Asp	Trp	Asp	Gln	Leu	Ala	Ser	Ala	Pro	Gln	Pro	Leu	Val	Leu	Gln	Ala	
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Arg	Val	Asp	Asp	Leu	Ser	Arg	Ile	Ala	Gln	Glu	Leu	Lys	Ala	Arg	Asn	
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Met	Ser	Leu	Glu	Thr	Pro	Val	Ser	Val	Thr	Ala	Asn	Gly	Thr	Thr	Arg	
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Leu	Gln	Arg	Thr	Tyr	Asp	Thr	Thr	Leu	Gly	Leu	Leu	His	Lys	Leu	Asp	
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Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val Asp	
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Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg Ala Leu Tyr Gly Trp	
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Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu Val Pro Thr Ile Ser	
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Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala Ile Lys Gly	
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Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser Val Asn Ala	
375 380 385	
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Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe Gly Leu Asp Ser Arg	
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Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys Thr Ala Ala	
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Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro Ala Arg Thr	
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Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu Tyr Phe Glu	
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Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala Asp Ile Ala	
455 460 465	
acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg gaa gtc gaa	1555
Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp Glu Val Glu	
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gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca agc gct gat	1603
Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro Ser Ala Asp	
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Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val Ala Phe Thr	
505 510 515	
tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt aaa cca cac	1699
Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly Lys Pro His	
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cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca gcg acc gct	1747

Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala Ala Thr Ala
 535 540 545

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 Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile Ala Glu Val
 550 555 560 565

cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat ctg cgc gct 1843
 Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp Leu Arg Ala
 570 575 580

aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt cga aaa gcg 1891
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<213> Corynebacterium glutamicum

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 35 40 45

Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50 55 60

Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65 70 75 80

Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
 85 90 95

Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
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Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
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Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
 130 135 140

Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
 145 150 155 160

Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
 165 170 175

Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190

Leu	Glu	Phe	Gln	Val	Val	Pro	Gly	Met	Ser	Leu	Pro	Ala	Thr	Val	Pro	195	200	205
Ala	Phe	Ala	Gly	Ile	Ala	Leu	Gly	Ser	Thr	Tyr	Thr	Glu	Thr	Asp	Val	210	215	220
Asn	Gly	Gln	Asn	Leu	Asp	Trp	Asp	Gln	Leu	Ala	Ser	Ala	Pro	Gln	Pro	225	230	235
Leu	Val	Leu	Gln	Ala	Arg	Val	Asp	Asp	Leu	Ser	Arg	Ile	Ala	Gln	Glu	245	250	255
Leu	Lys	Ala	Arg	Asn	Met	Ser	Leu	Glu	Thr	Pro	Val	Ser	Val	Thr	Ala	260	265	270
Asn	Gly	Thr	Thr	Arg	Leu	Gln	Arg	Thr	Tyr	Asp	Thr	Thr	Leu	Gly	Leu	275	280	285
Leu	His	Lys	Leu	Asp	Ala	Glu	Leu	Ser	Gly	Pro	Leu	Val	Val	Thr	Leu	290	295	300
Gly	Lys	Gly	Val	Asp	Asp	Arg	Ser	Lys	Tyr	Ser	Trp	Trp	Glu	Asn	Arg	305	310	315
Ala	Leu	Tyr	Gly	Trp	Arg	Val	Leu	Val	Pro	Arg	Ala	Arg	Glu	Gln	Ala	325	330	335
Ala	Ser	Met	Ser	Ala	Arg	Leu	Ser	Ser	His	Gly	Ala	Ile	Pro	Gln	Glu	340	345	350
Val	Pro	Thr	Ile	Ser	Val	Glu	Pro	Pro	Arg	Asn	Pro	Ala	Gln	Met	Glu	355	360	365
Arg	Ala	Ile	Lys	Gly	Ile	Val	Glu	Gly	Arg	Tyr	Gln	Trp	Val	Val	Leu	370	375	380
Thr	Ser	Val	Asn	Ala	Val	Lys	Ala	Val	Trp	Glu	Lys	Ile	Thr	Glu	Phe	385	390	395
Gly	Leu	Asp	Ser	Arg	Ser	Phe	Ala	Gly	Val	Arg	Ile	Ala	Ala	Val	Gly	405	410	415
Glu	Lys	Thr	Ala	Ala	Glu	Ile	Arg	Ala	Leu	Gly	Ile	Thr	Pro	Glu	Leu	420	425	430
Leu	Pro	Ala	Arg	Thr	Arg	Gln	Asn	Ala	Gln	Gly	Leu	Val	Asp	Val	Phe	435	440	445
Pro	Glu	Tyr	Phe	Glu	Glu	Leu	Asp	Pro	Val	Gly	Arg	Val	Leu	Leu	Pro	450	455	460
Arg	Ala	Asp	Ile	Ala	Thr	Asp	Val	Leu	Val	Asp	Gly	Leu	Thr	His	Leu	465	470	475
Gly	Trp	Glu	Val	Glu	Asp	Val	Val	Ala	Tyr	Arg	Thr	Val	Arg	Ala	Ala	485	490	495
Pro	Pro	Ser	Ala	Asp	Ile	Arg	Asp	Met	Ile	Lys	Thr	Gly	Gly	Phe	Asp	500	505	510

Ala Val Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile
 515 520 525

Ala Gly Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met
 530 535 540

Thr Ala Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro
 545 550 555 560

Glu Ile Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val
 565 570 575

Ala Asp Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg
 580 585 590

Arg Arg Arg Lys Ala Ser
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<210> 821

<211> 1024

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1024)

<223> FRXA00371

<400> 821

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acgttggtcg ttttcgagac aagtactaga aaagatattg atg act atc gcc cat 115
 Met Thr Ile Ala His
 1 5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser
 10 15 20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val
 25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro
 40 45 50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu
 55 60 65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr
 70 75 80 85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403
 Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile
 90 95 100

cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc 451

Pro	Val	Pro	Glu	Asp	Lys	Leu	Gln	Ala	Ala	Glu	Asp	Glu	Tyr	Glu	Arg		
			105					110					115				
atc	tgc	att	gaa	gcg	aag	gag	aac	ggg	gca	cgc	cgt	aag	cct	cct	cgt	499	
Ile	Cys	Ile	Glu	Ala	Lys	Glu	Asn	Gly	Ala	Arg	Arg	Lys	Pro	Pro	Arg		
		120					125					130					
cca	gca	cca	cca	acc	gct	gca	gag	atc	acg	gaa	gtt	tct	gag	gcg	act	547	
Pro	Ala	Pro	Pro	Thr	Ala	Ala	Glu	Ile	Thr	Glu	Val	Ser	Glu	Ala	Thr		
	135					140					145						
cca	gct	cag	att	gtt	gag	ctt	gtg	cag	gat	gct	ctt	tct	tat	ggg	gga	595	
Pro	Ala	Gln	Ile	Val	Glu	Leu	Val	Gln	Asp	Ala	Leu	Ser	Tyr	Gly	Gly		
150					155					160					165		
gat	gtt	att	cgt	ctt	gtc	acc	ggc	aac	cca	ttg	agc	agc	gat	gcc	aca	643	
Asp	Val	Ile	Arg	Leu	Val	Thr	Gly	Asn	Pro	Leu	Ser	Ser	Asp	Ala	Thr		
				170					175						180		
ctg	gct	gag	atc	tct	gca	gtt	tcc	gag	gct	ggc	ctg	gag	ttc	cag	gtg	691	
Leu	Ala	Glu	Ile	Ser	Ala	Val	Ser	Glu	Ala	Gly	Leu	Glu	Phe	Gln	Val		
				185				190					195				
gtt	cca	ggg	atg	tct	ttg	cct	gca	acg	gtt	cct	gca	ttt	gcg	gga	att	739	
Val	Pro	Gly	Met	Ser	Leu	Pro	Ala	Thr	Val	Pro	Ala	Phe	Ala	Gly	Ile		
		200					205					210					
gcg	ttg	ggg	tct	acc	tac	acc	gaa	act	gat	gtc	aac	ggg	caa	aac	ttg	787	
Ala	Leu	Gly	Ser	Thr	Tyr	Thr	Glu	Thr	Asp	Val	Asn	Gly	Gln	Asn	Leu		
	215					220					225						
gac	tgg	gat	cag	ttg	gct	agc	gca	cct	cag	cct	ttg	gtg	ctg	cag	gcc	835	
Asp	Trp	Asp	Gln	Leu	Ala	Ser	Ala	Pro	Gln	Pro	Leu	Val	Leu	Gln	Ala		
230					235					240					245		
cgc	gtg	gat	gac	ctt	tcc	cgt	att	gca	cag	gaa	cta	aag	gcc	cgc	aat	883	
Arg	Val	Asp	Asp	Leu	Ser	Arg	Ile	Ala	Gln	Glu	Leu	Lys	Ala	Arg	Asn		
				250					255					260			
atg	tct	ttg	gaa	act	cct	gtt	tct	gtc	acc	gct	aac	ggc	acc	acc	cgt	931	
Met	Ser	Leu	Glu	Thr	Pro	Val	Ser	Val	Thr	Ala	Asn	Gly	Thr	Thr	Arg		
			265					270					275				
ttg	cag	cgc	acc	tat	gac	acc	act	tta	ggg	ctg	ttg	cac	aag	ctt	gat	979	
Leu	Gln	Arg	Thr	Tyr	Asp	Thr	Thr	Leu	Gly	Leu	Leu	His	Lys	Leu	Asp		
		280					285					290					
gct	gaa	cta	agc	gga	cct	ttg	gtt	gtt	acc	ttg	ggc	aag	ggg	gtg		1024	
Ala	Glu	Leu	Ser	Gly	Pro	Leu	Val	Val	Thr	Leu	Gly	Lys	Gly	Val			
	295					300					305						

<210> 822

<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 822

Met	Thr	Ile	Ala	His	Lys	Pro	Glu	Met	Ala	Glu	Thr	Thr	Gly	Ile	Glu
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Thr Asn Gln Val Ser Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly
 20 25 30
 Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
 35 40 45
 Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50 55 60
 Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65 70 75 80
 Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
 85 90 95
 Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
 100 105 110
 Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
 115 120 125
 Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
 130 135 140
 Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
 145 150 155 160
 Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
 165 170 175
 Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300
 Gly Lys Gly Val
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<210> 823

<211> 755

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(732)

<223> FRXA00374

<400> 823

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atc aag ggc atc gtc gaa gga cgc tac cag tgg gtt gtc ctc aca agc	96
Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser	
20 25 30	
gtc aac gca gtg aag gca gtc tgg aag aaa atc acc gaa ttc ggc ctc	144
Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu	
35 40 45	
gat tca cgt tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa	192
Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys	
50 55 60	
acc gcc gct gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct	240
Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro	
65 70 75 80	
gca cgt acc agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa	288
Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu	
85 90 95	
tat ttc gaa gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca	336
Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala	
100 105 110	
gat atc gca acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg	384
Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp	
115 120 125	
gaa gtc gaa gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca	432
Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro	
130 135 140	
agc gct gat atc cga gat atg atc aag acc ggc gga ttt gat gca gtt	480
Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val	
145 150 155 160	
gcc ttc acc tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt	528
Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly	
165 170 175	
aaa cca cac cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca	576
Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala	
180 185 190	
gcg acc gct gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc	624
Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile	
195 200 205	
gcc gaa gta cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat	672

Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

ctg cgc gct aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt 720
 Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg
 225 230 235 240

cga aaa gcg tct taaaagggtt ttcactaggg tgt 755
 Arg Lys Ala Ser

<210> 824
 <211> 244
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 824
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Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser
 20 25 30

Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu
 35 40 45

Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys
 50 55 60

Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro
 65 70 75 80

Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu
 85 90 95

Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala
 100 105 110

Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp
 115 120 125

Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro
 130 135 140

Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val
 145 150 155 160

Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly
 165 170 175

Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala
 180 185 190

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile
 195 200 205

Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg

225

230

235

240

Arg Lys Ala Ser

<210> 825

<211> 1467

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1444)

<223> RXN00383

<400> 825

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 Met Arg Phe Ala Ile
 1 5

atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163
 Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys
 10 15 20

gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211
 Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile
 25 30 35

ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259
 Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile
 40 45 50

gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307
 Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe
 55 60 65

act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355
 Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys
 70 75 80 85

tct cag tat ttc gcg ggc ggt gcg ctg cat gcg ttc ccc gca ggt gga 403
 Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala Phe Pro Ala Gly Gly
 90 95 100

gtg atg ggt att cca agc aat cca cca gca ggc gcg caa gac acc gct 451
 Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly Ala Gln Asp Thr Ala
 105 110 115

ttt gat tgg act cct ggc caa gac att tct gtt ggc gcc tta gtg cgc 499
 Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val Gly Ala Leu Val Arg
 120 125 130

cgt cag tat ggc gat gag atc gtc gat act gtg gtg tct tcg ctg ctt 547
 Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val Val Ser Ser Leu Leu
 135 140 145

ggt ggc gtt tat tcc tcc acc gct gat gat ctg ggt gtg cgc gct tcc 595
 Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu Gly Val Arg Ala Ser

150	155	160	165	
gtg ccg gca ctt gct gca gcc ctt gat cag ctg gct gag gcc ggc gag	643			
Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu Ala Glu Ala Gly Glu				
170 175 180				
ccg gtg act ctg tca gct gcg gtc aag gcc gtg gaa gct cag cgg gaa	691			
Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val Glu Ala Gln Arg Glu				
185 190 195				
gcc gca aaa aca act tca gaa acc cgc ccc gtt ttc cag acc ttc aag	739			
Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val Phe Gln Thr Phe Lys				
200 205 210				
ggc gga tac gcg gag ctg tac gaa gcg ttg gca gag caa tgc ggt gca	787			
Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala Glu Gln Cys Gly Ala				
215 220 225				
gat att cac ttg gat agt ttc gtt tcc gcc atc acc aaa gat ggt gaa	835			
Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile Thr Lys Asp Gly Glu				
230 235 240 245				
ggg ttt gcc atc aag ggc ggt ggc gaa ggc acc tac gac aag gtg att	883			
Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr Tyr Asp Lys Val Ile				
250 255 260				
ttg gcg gtt ccc gct cca acc gcc gct gtg ctg ctc cgc gac ttg gca	931			
Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu Leu Arg Asp Leu Ala				
265 270 275				
ccg gcc gca gcg cca cat ttg cgc gca att aag ttg gct tct tca gca	979			
Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys Leu Ala Ser Ser Ala				
280 285 290				
gtc gtc ggc atg cgt ttc gat tcc agc gag ggc ctg ccc gac aac tcc	1027			
Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly Leu Pro Asp Asn Ser				
295 300 305				
ggc gtc ctg gtc gct gtt aat gag ccg ggc atc acg gcg aag gcc ttc	1075			
Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile Thr Ala Lys Ala Phe				
310 315 320 325				
acg ttc tcc tca aag aag tgg cct cac ctg gag gct cgc ggg ggc gcg	1123			
Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu Ala Arg Gly Gly Ala				
330 335 340				
ctc gtg cgc gcg tcg ttc ggc agg cta ggc gat gag gcg tcg gca cgc	1171			
Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp Glu Ala Ser Ala Arg				
345 350 355				
atg gac gag gat ttg ctt gtc gac gcc gcc ctc gac gat ctc ctc acc	1219			
Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu Asp Asp Leu Leu Thr				
360 365 370				
ata acc ggg ttc gac ggc cgg gct gcc gga ctg ggt gaa att ttc gtg	1267			
Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu Gly Glu Ile Phe Val				
375 380 385				
cag cgc tgg ttc ggt ggg ctc cca gcc tat gga gtt gat cac att gct	1315			
Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly Val Asp His Ile Ala				
390 395 400 405				

acc gtt tcg gct gcg cgt gca gag atc gca gcc gtg cct ggc gtg gaa 1363
 Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala Val Pro Gly Val Glu
 410 415 420

gca att ggc gcg tgg gct ggg gga gtg gga gtt ccc gca gtt atc gca 1411
 Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val Pro Ala Val Ile Ala
 425 430 435

gat gcc cag gca gca gta cac agg ttg ctg gga taagcacccca aaaacactat 1464
 Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
 440 445

tga 1467

<210> 826

<211> 448

<212> PRT

<213> Corynebacterium glutamicum

<400> 826

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 20 25 30

Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser
 35 40 45

Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp
 50 55 60

Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
 65 70 75 80

Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala
 85 90 95

Phe Pro Ala Gly Gly Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly
 100 105 110

Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val
 115 120 125

Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val
 130 135 140

Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu
 145 150 155 160

Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu
 165 170 175

Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val
 180 185 190

Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val
 195 200 205

Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala
 210 215 220
 Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile
 225 230 235 240
 Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr
 245 250 255
 Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu
 260 265 270
 Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys
 275 280 285
 Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly
 290 295 300
 Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile
 305 310 315 320
 Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu
 325 330 335
 Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp
 340 345 350
 Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu
 355 360 365
 Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu
 370 375 380
 Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly
 385 390 395 400
 Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala
 405 410 415
 Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val
 420 425 430
 Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
 435 440 445

<210> 827

<211> 382

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(382)

<223> FRXA00376

<400> 827

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                               Met Arg Phe Ala Ile
                               1           5

atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163
Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys
                10                15                20

gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211
Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile
                25                30                35

ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259
Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile
                40                45                50

gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307
Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe
                55                60                65

act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355
Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys
                70                75                80                85

tct cag tat ttc gcg ggc ggt gcg ctg 382
Ser Gln Tyr Phe Ala Gly Gly Ala Leu
                90

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<210> 828

<211> 94

<212> PRT

<213> Corynebacterium glutamicum

<400> 828

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Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu
    20           25           30

Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser
    35           40           45

Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp
    50           55           60

Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
    65           70           75           80

Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu
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<210> 829

<211> 1037

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1014)

<223> FRXA00383

<400> 829

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Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile	
1 5 10 15	
tct gtt ggc gcc tta gtg cgc cgt cag tat ggc gat gag atc gtc gat	96
Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp	
20 25 30	
act gtg gtg tct tcg ctg ctt ggt ggc gtt tat tcc tcc acc gct gat	144
Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp	
35 40 45	
gat ctg ggt gtg cgc gct tcc gtg ccg gca ctt gct gca gcc ctt gat	192
Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp	
50 55 60	
cag ctg gct gag gcc ggc gag ccg gtg act ctg tca gct gcg gtc aag	240
Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys	
65 70 75 80	
gcc gtg gaa gct cag cgg gaa gcc gca aaa aca act tca gaa acc cgc	288
Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg	
85 90 95	
ccc gtt ttc cag acc ttc aag ggc gga tac gcg gag ctg tac gaa gcg	336
Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala	
100 105 110	
ttg gca gag caa tgc ggt gca gat att cac ttg gat agt ttc gtt tcc	384
Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser	
115 120 125	
gcc atc acc aaa gat ggt gaa ggt ttt gcc atc aag ggc ggt ggc gaa	432
Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu	
130 135 140	
ggc acc tac gac aag gtg att ttg gcg gtt ccc gct cca acc gcc gct	480
Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala	
145 150 155 160	
gtg ctg ctg cgc gac ttg gca ccg gcc gca gcg cca cat ttg cgc gca	528
Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala	
165 170 175	
att aag ttg gct tct tca gca gtc gtc ggc atg cgt ttc gat tcc agc	576
Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser	
180 185 190	
gag ggc ctg ccc gac aac tcc ggc gtc ctg gtc gct gtt aat gag ccg	624
Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro	
195 200 205	
ggc atc acg gcg aag gcc ttc acg ttc tcc tca aag aag tgg cct cac	672
Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His	
210 215 220	

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ctg gag gct cgc ggg ggc gcg ctc gtg cgc gcg tcg ttc ggc agg cta 720
Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu
225                230                235                240

ggc gat gag gcg tcg gca cgc atg gac gag gat ttg ctt gtc gac gcc 768
Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala
                245                250                255

gcc ctc gac gat ctc ctc acc ata acc ggg ttc gac ggc cgg gct gcc 816
Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala
                260                265                270

gga ctg ggt gaa att ttc gtg cag cgc tgg ttc ggt ggg ctc cca gcc 864
Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala
                275                280                285

tat gga gtt gat cac att gct acc gtt tcg gct gcg cgt gca gag atc 912
Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile
                290                295                300

gca gcc gtg cct ggc gtg gaa gca att ggc gcg tgg gct ggg gga gtg 960
Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val
305                310                315                320

gga gtt ccc gca gtt atc gca gat gcc cag gca gca gta cac agg ttg 1008
Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu
                325                330                335

ctg gga taagcaccca aaaacactat tga 1037
Leu Gly

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<210> 830

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 830

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Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile
  1                5                10                15

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Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp
      20                25                30

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Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp
      35                40                45

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Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp
      50                55                60

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Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys
      65                70                75                80

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Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg
      85                90                95

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```

Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala
     100                105                110

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Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser

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115					120					125									
Ala	Ile	Thr	Lys	Asp	Gly	Glu	Gly	Phe	Ala	Ile	Lys	Gly	Gly	Gly	Glu				
130					135					140									
Gly	Thr	Tyr	Asp	Lys	Val	Ile	Leu	Ala	Val	Pro	Ala	Pro	Thr	Ala	Ala				
145					150					155					160				
Val	Leu	Leu	Arg	Asp	Leu	Ala	Pro	Ala	Ala	Ala	Pro	His	Leu	Arg	Ala				
165					170					175									
Ile	Lys	Leu	Ala	Ser	Ser	Ala	Val	Val	Gly	Met	Arg	Phe	Asp	Ser	Ser				
180					185					190									
Glu	Gly	Leu	Pro	Asp	Asn	Ser	Gly	Val	Leu	Val	Ala	Val	Asn	Glu	Pro				
195					200					205									
Gly	Ile	Thr	Ala	Lys	Ala	Phe	Thr	Phe	Ser	Ser	Lys	Lys	Trp	Pro	His				
210					215					220									
Leu	Glu	Ala	Arg	Gly	Gly	Ala	Leu	Val	Arg	Ala	Ser	Phe	Gly	Arg	Leu				
225					230					235					240				
Gly	Asp	Glu	Ala	Ser	Ala	Arg	Met	Asp	Glu	Asp	Leu	Leu	Val	Asp	Ala				
245					250					255									
Ala	Leu	Asp	Asp	Leu	Leu	Thr	Ile	Thr	Gly	Phe	Asp	Gly	Arg	Ala	Ala				
260					265					270									
Gly	Leu	Gly	Glu	Ile	Phe	Val	Gln	Arg	Trp	Phe	Gly	Gly	Leu	Pro	Ala				
275					280					285									
Tyr	Gly	Val	Asp	His	Ile	Ala	Thr	Val	Ser	Ala	Ala	Arg	Ala	Glu	Ile				
290					295					300									
Ala	Ala	Val	Pro	Gly	Val	Glu	Ala	Ile	Gly	Ala	Trp	Ala	Gly	Gly	Val				
305					310					315					320				
Gly	Val	Pro	Ala	Val	Ile	Ala	Asp	Ala	Gln	Ala	Ala	Val	His	Arg	Leu				
325					330					335									

Leu Gly

<210> 831

<211> 873

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (850)

<223> RXA01253

<400> 831

acgccatcgc agcctgccct cctggccgca tcgaagtcct cgccaactac accgcattcc 60

gagacctcaa aaaggctctg gagaaaggga ccgaacaata atg acc acc ctc aac 115

Met Thr Thr Leu Asn

1

5

atc ggc ctc atc ctc ccc gac gtc ctc gga act tac ggc gac gac ggc	163
Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr Tyr Gly Asp Asp Gly	
10 15 20	
aac gca cta gtc ctg cgc caa cgc gca cgc atg cgt ggc att aat gct	211
Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met Arg Gly Ile Asn Ala	
25 30 35	
gaa atc cag cgc gtc acc ctc gac gac gcc gtc cct tcc acc ctt gat	259
Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val Pro Ser Thr Leu Asp	
40 45 50	
ctc tac tgc ctc ggc ggc ggc gag gac acc gca cag atc ctt gcc acc	307
Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala Gln Ile Leu Ala Thr	
55 60 65	
gaa cac ctc acc aaa gac ggc ggc ctc caa acc gca gcc gcc gca ggc	355
Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr Ala Ala Ala Ala Gly	
70 75 80 85	
cgc ccc atc ttc gca gtc tgc gca ggt ctc cag gta ctc ggc gac tcc	403
Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln Val Leu Gly Asp Ser	
90 95 100	
ttc cgc gcc gcc ggc cgt gtc atc gac ggc ctt ggg ctt atc gac gcc	451
Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu Gly Leu Ile Asp Ala	
105 110 115	
acc acc gtc tct tta caa aaa cgc gcc atc gga gaa gtc gaa acg aca	499
Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly Glu Val Glu Thr Thr	
120 125 130	
cca acc cgc gcc gga ttc acc gcc gag ctg acc gaa cga ctc acc ggc	547
Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr Glu Arg Leu Thr Gly	
135 140 145	
ttc gaa aac cac atg ggc gcc acc ctg ctc ggc ccc gac gcc gaa cca	595
Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly Pro Asp Ala Glu Pro	
150 155 160 165	
ctc ggc cga gtc gtc cgc ggc gaa ggc aac acc gat gtc tgg gca gcc	643
Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr Asp Val Trp Ala Ala	
170 175 180	
tcc gaa aac acc gac gac caa cgc caa caa ttc gcc gaa ggc gcc gtc	691
Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe Ala Glu Gly Ala Val	
185 190 195	
caa ggc agc atc atc gcc acc tac atg cac ggc ccc gca ctc gcc cga	739
Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly Pro Ala Leu Ala Arg	
200 205 210	
aac ccc caa ctc gcc gac ctc atg ctc gca aaa gca atg ggt gtc gcg	787
Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys Ala Met Gly Val Ala	
215 220 225	
ctg aaa gac ctg gag cct ttg gac atc gac gtc atc gac cgc ctc cgc	835
Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val Ile Asp Arg Leu Arg	
230 235 240 245	

gcc gaa cgc ctg gcg tagcccccttc taaaccgggt cta
 Ala Glu Arg Leu Ala
 250

873

<210> 832

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 832

Met Thr Thr Leu Asn Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr
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Tyr Gly Asp Asp Gly Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met
 20 25 30

Arg Gly Ile Asn Ala Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val
 35 40 45

Pro Ser Thr Leu Asp Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala
 50 55 60

Gln Ile Leu Ala Thr Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr
 65 70 75 80

Ala Ala Ala Ala Gly Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln
 85 90 95

Val Leu Gly Asp Ser Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu
 100 105 110

Gly Leu Ile Asp Ala Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly
 115 120 125

Glu Val Glu Thr Thr Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr
 130 135 140

Glu Arg Leu Thr Gly Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly
 145 150 155 160

Pro Asp Ala Glu Pro Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr
 165 170 175

Asp Val Trp Ala Ala Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe
 180 185 190

Ala Glu Gly Ala Val Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly
 195 200 205

Pro Ala Leu Ala Arg Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys
 210 215 220

Ala Met Gly Val Ala Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val
 225 230 235 240

Ile Asp Arg Leu Arg Ala Glu Arg Leu Ala
 245 250

<210> 833

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<220>  
<221> CDS  
<222> (101)..(1021)  
<223> RXA02134
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tgatgaacga catgtcgaca ttttcttccg ccggcgtcga tggaccccta aacgcctctt 60

aaa aac cac aac gcc ttc tcc ccc acc ggc ttt ggc gca cta gtc atc 691

Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe Gly Ala Leu Val Ile
 185 190 195
 gga acg gtg aaa ttt tgg tgg atc gcg ctg tgg ctc ttg gtt act gct 739
 Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp Leu Leu Val Thr Ala
 200 205 210
 gcg ttg gct ttt tgg tgc gca gaa tta att tct cca ctt tca ccg ctg 787
 Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser Pro Leu Ser Pro Leu
 215 220 225
 acc agt gtt aac act ccc ttt gtc gct gga cct ttc ccc gct gca atc 835
 Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro Phe Pro Ala Ala Ile
 230 235 240 245
 aac ccc gcc tgg ctt gga ggc tgg gtt gcg ata acc gca gtc gtg gca 883
 Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile Thr Ala Val Val Ala
 250 255 260
 tgt gtt ttc gca gca ctt ttc agc cgc cgc tta tca cga agt ttc ggt 931
 Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu Ser Arg Ser Phe Gly
 265 270 275
 gga ctc aac gga gac tgc atc ggc gca tgc att cat ctc ggg gcg tcg 979
 Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile His Leu Gly Ala Ser
 280 285 290
 att tct gca gtg atg ttt gct gtt gtc gcc aat gca atg gtg 1021
 Ile Ser Ala Val Met Phe Ala Val Val Ala Asn Ala Met Val
 295 300 305
 taaagcgggtg gcgtcttttg gga 1044

 <210> 834
 <211> 307
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 834
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 Asn Arg His Gly Asn Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn
 20 25 30
 Trp Met Thr Val Leu Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr
 35 40 45
 Thr Gly Ala Arg Val Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe
 50 55 60
 Gly Met Phe Thr Ala Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly
 65 70 75 80
 Val Ile His Val Asp Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe
 85 90 95
 Trp Glu Leu Leu Asn Arg Phe Met His Leu Asp Gly Leu Ala Asp Val
 100 105 110

Ser Asp Ala Leu Gly Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile
 115 120 125
 Leu Ala Asp Pro Arg Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu
 130 135 140
 Ser Val Leu Leu Gln Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr
 145 150 155 160
 Val Trp Trp Met Ile Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly
 165 170 175
 Gln Val Thr Ala Leu Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe
 180 185 190
 Gly Ala Leu Val Ile Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp
 195 200 205
 Leu Leu Val Thr Ala Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser
 210 215 220
 Pro Leu Ser Pro Leu Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro
 225 230 235 240
 Phe Pro Ala Ala Ile Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile
 245 250 255
 Thr Ala Val Val Ala Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu
 260 265 270
 Ser Arg Ser Phe Gly Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile
 275 280 285
 His Leu Gly Ala Ser Ile Ser Ala Val Met Phe Ala Val Val Ala Asn
 290 295 300
 Ala Met Val
 305

<210> 835

<211> 1197

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1174)

<223> RXA02135

<400> 835

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aaaacgtttt aagaaaacag tcggtttgaa ggagttgtta atg gtt cca gca gag 115
 Met Val Pro Ala Glu
 1 5

ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg 163
 Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr
 10 15 20

aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag	211
Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys	
25 30 35	
ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg	259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro	
40 45 50	
cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac	307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His	
55 60 65	
ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg	355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu	
70 75 80 85	
cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att	403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile	
90 95 100	
gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac	451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp	
105 110 115	
cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc	499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile	
120 125 130	
gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag	547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys	
135 140 145	
atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att	595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile	
150 155 160 165	
tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc	643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala	
170 175 180	
ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc	691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg	
185 190 195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc	739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile	
200 205 210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc	787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala	
215 220 225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc	835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe	
230 235 240 245	
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt	883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val	
250 255 260	
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc	931

Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala
 265 270 275

agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc 979
 Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser
 280 285 290

gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg 1027
 Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met
 295 300 305

tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag 1075
 Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys
 310 315 320 325

att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc 1123
 Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly
 330 335 340

gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg 1171
 Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr
 345 350 355

gag taacttttcta agcgatgtcc ggc 1197
 Glu

<210> 836
 <211> 358
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 836
 Met Val Pro Ala Glu Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys
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Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro
 20 25 30

Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
 35 40 45

Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
 50 55 60

Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
 65 70 75 80

Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
 85 90 95

Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
 100 105 110

Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
 115 120 125

Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
 130 135 140

Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
 145 150 155 160
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
 165 170 175
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
 180 185 190
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
 195 200 205
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
 210 215 220
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
 225 230 235 240
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
 245 250 255
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
 260 265 270
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
 275 280 285
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
 290 295 300
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
 305 310 315 320
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
 325 330 335
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala
 340 345 350
 Pro Glu Gln Asn Thr Glu
 355

<210> 837
 <211> 645
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(622)
 <223> RXA02136

<400> 837
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 ccctcgtgca cgcggttgaaa ttggtgctga agtctagcgc atg cgc acg tta gtt 115
 Met Arg Thr Leu Val
 1 5
 ctt ggc ggg gcc agg tct ggt aag tct gct ttt gca gaa tca ctt gtt 163

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Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe Ala Glu Ser Leu Val
      10                      15                      20

gga tct ggt ccc gtt ttg tat gtc gca acg gca agg cct tcg gga gat 211
Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala Arg Pro Ser Gly Asp
      25                      30                      35

gat cct gaa ttc gcc gag cgc att gcg gtt cat gcg gag cgg cgc cca 259
Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His Ala Glu Arg Arg Pro
      40                      45                      50

acg tct tgg gtg ttg gac gag gag ggg gac gtc gat aag ctt ctt gcc 307
Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val Asp Lys Leu Leu Ala
      55                      60                      65

tcg cca ccg gcc atg ccg gtg ctc gtt gat gac ctg ggc acc tgg ctc 355
Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp Leu Gly Thr Trp Leu
      70                      75                      80                      85

acg cac gcc acc gat gcg tgc gac ggt tgg gag gcg agt tcg gcg cag 403
Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu Ala Ser Ser Ala Gln
      90                      95                      100

ctt gag gcc aag atg gat ttg ctt atc gac gcc atc ctc cac ttt cag 451
Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala Ile Leu His Phe Gln
      105                      110                      115

ggc gaa gat ctg gta att gtt tca cct gaa gtt ggt atg gga atc gtc 499
Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val Gly Met Gly Ile Val
      120                      125                      130

ccg gaa tat aaa tct ggg cgc ctt ttt cgt gat cgc atc ggc aca ctt 547
Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp Arg Ile Gly Thr Leu
      135                      140                      145

aat cag cgt gtc gca gcg att tgc gag agg gtt gtc ttc gtg gtt gct 595
Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val Val Phe Val Val Ala
      150                      155                      160                      165

ggg ctg cca cta gag ttg aaa acg ttt taagaaaaca gtcggtttga 642
Gly Leu Pro Leu Glu Leu Lys Thr Phe
      170

agg 645

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<210> 838

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 838

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Met Arg Thr Leu Val Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe
  1                      5                      10                      15

Ala Glu Ser Leu Val Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala
      20                      25                      30

Arg Pro Ser Gly Asp Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His
      35                      40                      45

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Ala Glu Arg Arg Pro Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val
 50 55 60

Asp Lys Leu Leu Ala Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp
 65 70 75 80

Leu Gly Thr Trp Leu Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu
 85 90 95

Ala Ser Ser Ala Gln Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala
 100 105 110

Ile Leu His Phe Gln Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val
 115 120 125

Gly Met Gly Ile Val Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp
 130 135 140

Arg Ile Gly Thr Leu Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val
 145 150 155 160

Val Phe Val Val Ala Gly Leu Pro Leu Glu Leu Lys Thr Phe
 165 170

<210> 839

<211> 575

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(552)

<223> RXN03114

<400> 839

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Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val	
1 5 10 15	
cgc cgc gag ttg acg gtg ggg ttg gat gct ggt gac ggt ccg att tta	96
Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu	
20 25 30	
agg cag agc ttt gat gtt ggt ttt ttg ctt gtc gac gcc tcc ttc cac	144
Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His	
35 40 45	
att cat atc aat ggc gtg tct act ggg cag tcg gtt gcg ccg gat gat	192
Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp	
50 55 60	
gta gtt gag gtg gtg cgt ggt ttg gct gat gct tcg gag ttg tcc gtg	240
Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val	
65 70 75 80	
gaa agt gtt gct gag ttg tgt act ccc gtg gca ccg gtt tca tta tct	288
Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser	
85 90 95	
gag gca cag ggg aat cct gcg cct att ggg tgg ttg gag cat gat ggc	336

Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly
 100 105 110
 gtg gtg tcg ttg ggt gcg ggt att cca ggg ggg cgg gtg gag gct cgt 384
 Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg
 115 120 125
 tta gcg cgt ttt att gcg gtg att gag gcg gag acc act att acc cca 432
 Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro
 130 135 140
 tgg aat tcg ttg atc att cat gat ttg tat gag ggt gtt gca gaa cag 480
 Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln
 145 150 155 160
 gtg gtg aag gtt ctg gct ccc atg ggg ttg gtt ttt gat gct aat tca 528
 Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser
 165 170 175
 ccg ctt ctg gag tca ccg gct ttg taactcgcca ttggtgcacg tct 575
 Pro Leu Leu Glu Ser Pro Ala Leu
 180

<210> 840

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 840

Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val
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 Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu
 20 25 30
 Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His
 35 40 45
 Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp
 50 55 60
 Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val
 65 70 75 80
 Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser
 85 90 95
 Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly
 100 105 110
 Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg
 115 120 125
 Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro
 130 135 140
 Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln
 145 150 155 160
 Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser

165

170

175

Pro Leu Leu Glu Ser Pro Ala Leu
180

<210> 841

<211> 1200

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1177)

<223> RXN01810

<400> 841

ccaccaccac aatgttgctc atcctcgcgg cggttcgttgt cgcaggtggc tccatgactc 60

gcttcaccgt cggcaaccgc actggaaaat aaggcttcac atg aat aac gct ttt 115
Met Asn Asn Ala Phe
1 5

cga cgc acc ctt aca tcc gta gtc ctc gcc gct agc ttg gcc tta acg 163
Arg Arg Thr Leu Thr Ser Val Val Leu Ala Ala Ser Leu Ala Leu Thr
10 15 20

gcc tgc gca agc tgg gat tca cct acg gca tct tcc aat ggt gat ctg 211
Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser Ser Asn Gly Asp Leu
25 30 35

att gag gag atc cag gca agc tcc acc tca aca gat ccg cgc acc ttc 259
Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr Asp Pro Arg Thr Phe
40 45 50

aca ggc ttg agc atc gtg gaa gat atc ggc gat gtg gtt ccc gta acc 307
Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp Val Val Pro Val Thr
55 60 65

gac aac gcc tca cca gct ctg cca gtt tct ttg acc gac gct gat ggc 355
Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu Thr Asp Ala Asp Gly
70 75 80 85

aac gac gtg gtg gtg gag aac gtg tcc cgc atc ctc cca ctg gat ctc 403
Asn Asp Val Val Val Glu Asn Val Ser Arg Ile Leu Pro Leu Asp Leu
90 95 100

tac gga acc tat tcc aaa acc atc gct ggc ctg gga ctc gtg gac aat 451
Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu Gly Leu Val Asp Asn
105 110 115

att gtg ggt cgt act gtt agt tcc acc gag cct gca ttg gcg gac att 499
Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro Ala Leu Ala Asp Ile
120 125 130

gag gtg gtc acc act ggc gga cac acc ctc aat gct gaa gcg atc ctt 547
Glu Val Val Thr Thr Gly Gly His Thr Leu Asn Ala Glu Ala Ile Leu
135 140 145

aat tta cat ccg act ttg gtg atc atc gac cac tcg atc ggc cca cgc 595
Asn Leu His Pro Thr Leu Val Ile Ile Asp His Ser Ile Gly Pro Arg

150	155	160	165	
gaa gtc atc gat	cag atc cgc gca gct ggt	gtc gcc acg gtg atc atg	643	
Glu Val Ile Asp	Gln Ile Arg Ala Ala Gly	Val Ala Thr Val Ile Met		
	170	175	180	
tcg ccg cag cgt	tcc att gcc tca att ggc	gac gac atc cgc gac atc	691	
Ser Pro Gln Arg	Ser Ile Ala Ser Ile	Gly Asp Asp Ile Arg Asp Ile		
	185	190	195	
gcc tcc gtc gtt	gga ctt cct gaa gaa ggg	gag aag ctc gcg gaa cgt	739	
Ala Ser Val Val	Gly Leu Pro Glu Glu Gly	Glu Lys Leu Ala Glu Arg		
	200	205	210	
tcc gtt gct gaa gtc	gaa gag gcc agc acg gtt	gtc gat gaa ctc acc	787	
Ser Val Ala Glu Val	Glu Glu Ala Ser Thr Val	Val Val Asp Glu Leu Thr		
	215	220	225	
cca gaa gat ccc ctc	aaa atg gta ttc ctc tat	gcc cgc gga act ggt	835	
Pro Glu Asp Pro Leu	Lys Met Val Phe Leu Tyr	Ala Arg Gly Thr Gly		
	230	235	240	
gga gtg ttc ttc att	ttg ggc gat gcc tat	ggt gga cgc gat ctc att	883	
Gly Val Phe Phe Ile	Leu Gly Asp Ala Tyr Gly	Gly Gly Arg Asp Leu Ile		
	250	255	260	
gaa ggc ctg ggc ggc	gtc gac atg gct gct gaa	aag ggc atc atg gat	931	
Glu Gly Leu Gly Gly	Val Asp Met Ala Ala Glu	Lys Gly Ile Met Asp		
	265	270	275	
ctg gca cca gcc aac	gcg gaa gca ctt gcc	gaa cta aat cca gac gtc	979	
Leu Ala Pro Ala Asn	Ala Glu Ala Leu Ala Glu	Leu Asn Pro Asp Val		
	280	285	290	
ttc gtg atg atg tcg	gaa gga cta gtc tcg	aca gga ggt atc gac ggt	1027	
Phe Val Met Met Ser	Glu Gly Leu Val Ser Thr	Gly Gly Ile Asp Gly		
	295	300	305	
ctt atg gaa cgc ccc	ggc att gct cag aca acc	gcc gga caa aac caa	1075	
Leu Met Glu Arg Pro	Gly Ile Ala Gln Thr Thr	Ala Gly Gln Asn Gln		
	310	315	320	
cga gta ctg gcg ctt	ccc gat ggt caa tca ttg	gcc ttt ggt gcc caa	1123	
Arg Val Leu Ala Leu	Pro Asp Gly Gln Ser Leu	Ala Phe Gly Ala Gln		
	330	335	340	
act ggc gag ttg ttg	ctc cgc gca tcc cgc	gaa ctg tat gtg cag ggc	1171	
Thr Gly Glu Leu Leu	Leu Arg Ala Ser Arg	Glu Leu Tyr Val Gln Gly		
	345	350	355	
ggc gag tagatgggtg	tgaaggaggt tga		1200	
Gly Glu				

<210> 842

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 842

Met	Asn	Asn	Ala	Phe	Arg	Arg	Thr	Leu	Thr	Ser	Val	Val	Leu	Ala	Ala	1	5	10	15
Ser	Leu	Ala	Leu	Thr	Ala	Cys	Ala	Ser	Trp	Asp	Ser	Pro	Thr	Ala	Ser	20	25	30	
Ser	Asn	Gly	Asp	Leu	Ile	Glu	Glu	Ile	Gln	Ala	Ser	Ser	Thr	Ser	Thr	35	40	45	
Asp	Pro	Arg	Thr	Phe	Thr	Gly	Leu	Ser	Ile	Val	Glu	Asp	Ile	Gly	Asp	50	55	60	
Val	Val	Pro	Val	Thr	Asp	Asn	Ala	Ser	Pro	Ala	Leu	Pro	Val	Ser	Leu	65	70	75	80
Thr	Asp	Ala	Asp	Gly	Asn	Asp	Val	Val	Val	Glu	Asn	Val	Ser	Arg	Ile	85	90	95	
Leu	Pro	Leu	Asp	Leu	Tyr	Gly	Thr	Tyr	Ser	Lys	Thr	Ile	Ala	Gly	Leu	100	105	110	
Gly	Leu	Val	Asp	Asn	Ile	Val	Gly	Arg	Thr	Val	Ser	Ser	Thr	Glu	Pro	115	120	125	
Ala	Leu	Ala	Asp	Ile	Glu	Val	Val	Thr	Thr	Gly	Gly	His	Thr	Leu	Asn	130	135	140	
Ala	Glu	Ala	Ile	Leu	Asn	Leu	His	Pro	Thr	Leu	Val	Ile	Ile	Asp	His	145	150	155	160
Ser	Ile	Gly	Pro	Arg	Glu	Val	Ile	Asp	Gln	Ile	Arg	Ala	Ala	Gly	Val	165	170	175	
Ala	Thr	Val	Ile	Met	Ser	Pro	Gln	Arg	Ser	Ile	Ala	Ser	Ile	Gly	Asp	180	185	190	
Asp	Ile	Arg	Asp	Ile	Ala	Ser	Val	Val	Gly	Leu	Pro	Glu	Glu	Gly	Glu	195	200	205	
Lys	Leu	Ala	Glu	Arg	Ser	Val	Ala	Glu	Val	Glu	Glu	Ala	Ser	Thr	Val	210	215	220	
Val	Asp	Glu	Leu	Thr	Pro	Glu	Asp	Pro	Leu	Lys	Met	Val	Phe	Leu	Tyr	225	230	235	240
Ala	Arg	Gly	Thr	Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Asp	Ala	Tyr	Gly	245	250	255	
Gly	Arg	Asp	Leu	Ile	Glu	Gly	Leu	Gly	Gly	Val	Asp	Met	Ala	Ala	Glu	260	265	270	
Lys	Gly	Ile	Met	Asp	Leu	Ala	Pro	Ala	Asn	Ala	Glu	Ala	Leu	Ala	Glu	275	280	285	
Leu	Asn	Pro	Asp	Val	Phe	Val	Met	Met	Ser	Glu	Gly	Leu	Val	Ser	Thr	290	295	300	
Gly	Gly	Ile	Asp	Gly	Leu	Met	Glu	Arg	Pro	Gly	Ile	Ala	Gln	Thr	Thr	305	310	315	320
Ala	Gly	Gln	Asn	Gln	Arg	Val	Leu	Ala	Leu	Pro	Asp	Gly	Gln	Ser	Leu				

325 330 335

Ala Phe Gly Ala Gln Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu
340 345 350

Leu Tyr Val Gln Gly Gly Glu
355

<210> 843
<211> 963
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (1)..(933)
<223> RXS03205

<400> 843

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Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro	
1 5 10 15	
gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg	96
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val	
20 25 30	
gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat	144
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp	
35 40 45	
cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	
gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa	480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu	
145 150 155 160	
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag	528


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Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
      165                      170                      175

tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc   576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
      180                      185                      190

acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc   624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
      195                      200                      205

ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat   672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
      210                      215                      220

gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc   720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
      225                      230                      235                      240

acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc   768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
      245                      250                      255

atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg   816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
      260                      265                      270

gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac   864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
      275                      280                      285

ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg   912
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
      290                      295                      300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aagccgtttt   963
Pro Ala Asp Leu Leu Asp Ser
      305                      310

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<210> 844

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 844

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Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
  1                      5                      10                      15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
      20                      25                      30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
      35                      40                      45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
      50                      55                      60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
      65                      70                      75                      80

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Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95
 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125
 Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140
 Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160
 Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175
 Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190
 Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205
 Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 845

<211> 956

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(933)

<223> FRXA00306

<400> 845

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 Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

48

gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg	96
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val	
20 25 30	
gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat	144
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp	
35 40 45	
cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	
gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa	480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu	
145 150 155 160	
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag	528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln	
165 170 175	
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc	576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg	
180 185 190	
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc	624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg	
195 200 205	
ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat	672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp	
210 215 220	
gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc	720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg	
225 230 235 240	
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc	768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser	
245 250 255	
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg	816

Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270

gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285

ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag 956
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 846

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 846

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80

Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95

Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110

Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125

Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140

Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160

Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175

Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190

Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205

Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 847
 <211> 819
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(796)
 <223> RXC01715

<400> 847
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 Val Ser Glu Leu Asp
 1 5
 att aaa cag ctc aac aaa ctg cag cgc tac tct cag tgg gcg gtg ttc 163
 Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser Gln Trp Ala Val Phe
 10 15 20
 cgt gct att cct gga gcg ctc gat gat gat cgc aca gaa gtc act gac 211
 Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg Thr Glu Val Thr Asp
 25 30 35
 caa gca gcc aag ttc ttt gcc gac ctt gaa gca gaa ggc aaa gtc act 259
 Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala Glu Gly Lys Val Thr
 40 45 50
 gtc cgt ggc att tac aac gcc tcc ggc ctg cgc gca gac gct gac tac 307
 Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg Ala Asp Ala Asp Tyr
 55 60 65
 atg atc tgg tgg cac gca gaa gaa ttc gaa gac att cag aag gcc ttc 355
 Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp Ile Gln Lys Ala Phe
 70 75 80 85
 gct gat ttc cgc cgc acc acc att ttg ggt cag gtt tct gag gtc ttc 403
 Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln Val Ser Glu Val Phe

90										95					100					
tgg	atc	gga	aac	gct	ctc	cac	cgt	cca	tct	gag	ttc	aac	aag	gct	cac	451				
Trp	Ile	Gly	Asn	Ala	Leu	His	Arg	Pro	Ser	Glu	Phe	Asn	Lys	Ala	His					
105							110					115								
ttg	cct	tca	ttc	atc	atg	ggt	gaa	gaa	gca	aag	gac	tgg	atc	act	gtt	499				
Leu	Pro	Ser	Phe	Ile	Met	Gly	Glu	Glu	Ala	Lys	Asp	Trp	Ile	Thr	Val					
120							125					130								
tac	ccg	ttc	gtg	cgc	agc	tac	gac	tgg	tac	atc	atg	gag	ccc	ttg	aag	547				
Tyr	Pro	Phe	Val	Arg	Ser	Tyr	Asp	Trp	Tyr	Ile	Met	Glu	Pro	Leu	Lys					
135							140					145								
cgt	tcc	cgc	att	ctc	cgc	gag	cac	gga	caa	gct	gct	gtg	gaa	ttc	cca	595				
Arg	Ser	Arg	Ile	Leu	Arg	Glu	His	Gly	Gln	Ala	Ala	Val	Glu	Phe	Pro					
150					155					160					165					
gat	gtt	cgt	gcc	aac	act	gtg	ccg	gct	ttc	gca	ctg	ggt	gac	tac	gaa	643				
Asp	Val	Arg	Ala	Asn	Thr	Val	Pro	Ala	Phe	Ala	Leu	Gly	Asp	Tyr	Glu					
170							175					180								
tgg	gtg	ctg	gct	ttc	gag	gct	gat	gag	ttg	cac	cgc	att	gtc	gat	ttg	691				
Trp	Val	Leu	Ala	Phe	Glu	Ala	Asp	Glu	Leu	His	Arg	Ile	Val	Asp	Leu					
185							190					195								
atg	cac	aag	atg	cgt	tac	acc	gag	gct	cgc	ctc	cac	gtc	cgt	gag	gag	739				
Met	His	Lys	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Leu	His	Val	Arg	Glu	Glu					
200							205					210								
ctg	cca	ttt	att	tct	gga	cag	cgc	gtc	gac	att	gca	gat	ctg	att	aag	787				
Leu	Pro	Phe	Ile	Ser	Gly	Gln	Arg	Val	Asp	Ile	Ala	Asp	Leu	Ile	Lys					
215					220					225										
gtt	ctt	cct	taaaagctgc	ttttctaaac	gat											819				
Val	Leu	Pro																		
230																				

<210> 848

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 848

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Gln	Trp	Ala	Val	Phe	Arg	Ala	Ile	Pro	Gly	Ala	Leu	Asp	Asp	Asp	Arg
			20					25					30		

Thr	Glu	Val	Thr	Asp	Gln	Ala	Ala	Lys	Phe	Phe	Ala	Asp	Leu	Glu	Ala
		35					40					45			

Glu	Gly	Lys	Val	Thr	Val	Arg	Gly	Ile	Tyr	Asn	Ala	Ser	Gly	Leu	Arg
	50					55					60				

Ala	Asp	Ala	Asp	Tyr	Met	Ile	Trp	Trp	His	Ala	Glu	Glu	Phe	Glu	Asp
65					70					75				80	

Ile	Gln	Lys	Ala	Phe	Ala	Asp	Phe	Arg	Arg	Thr	Thr	Ile	Leu	Gly	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85					90					95					
Val	Ser	Glu	Val	Phe	Trp	Ile	Gly	Asn	Ala	Leu	His	Arg	Pro	Ser	Glu
			100					105					110		
Phe	Asn	Lys	Ala	His	Leu	Pro	Ser	Phe	Ile	Met	Gly	Glu	Glu	Ala	Lys
		115					120					125			
Asp	Trp	Ile	Thr	Val	Tyr	Pro	Phe	Val	Arg	Ser	Tyr	Asp	Trp	Tyr	Ile
	130					135					140				
Met	Glu	Pro	Leu	Lys	Arg	Ser	Arg	Ile	Leu	Arg	Glu	His	Gly	Gln	Ala
145					150					155					160
Ala	Val	Glu	Phe	Pro	Asp	Val	Arg	Ala	Asn	Thr	Val	Pro	Ala	Phe	Ala
				165					170					175	
Leu	Gly	Asp	Tyr	Glu	Trp	Val	Leu	Ala	Phe	Glu	Ala	Asp	Glu	Leu	His
		180						185					190		
Arg	Ile	Val	Asp	Leu	Met	His	Lys	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Leu
		195					200					205			
His	Val	Arg	Glu	Glu	Leu	Pro	Phe	Ile	Ser	Gly	Gln	Arg	Val	Asp	Ile
	210					215					220				
Ala	Asp	Leu	Ile	Lys	Val	Leu	Pro								
225					230										

<210> 849

<211> 1587

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1564)

<223> RXN00420

<400> 849

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ttcaccacct	gaaaattttc	gggggtaacc	tttaaaggcg	atg	aac	agt	tct	cac		115
				Met	Asn	Ser	Ser	His		
				1				5		

ggc	acg	tcc	agc	tcc	ggc	gct	tcg	gcc	ggc	cac	gga	gcc	ctt	ccc	163
Gly	Thr	Ser	Ser	Ser	Gly	Ala	Ser	Ala	Gly	Ala	His	Gly	Ala	Leu	Pro
			10					15					20		

cta	gaa	gct	cag	aaa	ctg	aac	ggc	tgg	ggc	cgc	aca	gcc	ccc	acc	acc	211
Leu	Glu	Ala	Gln	Lys	Leu	Asn	Gly	Trp	Gly	Arg	Thr	Ala	Pro	Thr	Thr	
			25				30					35				

gct	gag	gta	ctt	acc	acc	cca	gac	cta	gac	atc	att	gtg	gat	gca	gtc	259
Ala	Glu	Val	Leu	Thr	Thr	Pro	Asp	Leu	Asp	Ile	Ile	Val	Asp	Ala	Val	
		40					45					50				

cgc	caa	gtc	gct	gaa	caa	aac	gac	tcc	aag	ccg	gac	tac	ctc	aag	cgc	307
Arg	Gln	Val	Ala	Glu	Gln	Asn	Asp	Ser	Lys	Pro	Asp	Tyr	Leu	Lys	Arg	

55	60	65	
ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa			355
Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln			
70	75	80	85
aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac			403
Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His			
	90	95	100
tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc			451
Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr			
	105	110	115
ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct			499
Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro			
	120	125	130
gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca			547
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro			
	135	140	145
gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac			595
Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His			
	150	155	160
gtg gtc tcc atg gaa ctc ctc gtt gca gac gga cgc atc ctg cac ctc			643
Val Val Ser Met Glu Leu Leu Val Ala Asp Gly Arg Ile Leu His Leu			
	170	175	180
gag cca gaa ggc acc gcc gaa gac cca cag ggc gac ctg ttc tgg gca			691
Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly Asp Leu Phe Trp Ala			
	185	190	195
acc gtt ggt ggc atg ggc ctg acc ggc atc atc gtc cgt gca cgc atc			739
Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile Val Arg Ala Arg Ile			
	200	205	210
cgc atg acc aag acg gaa acc gcc tac ttc att gcg gac acc gac cgc			787
Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile Ala Asp Thr Asp Arg			
	215	220	225
acc aac aac ttg gaa gaa acc gtt gcg ttc cac tcc gac gga tca gag			835
Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His Ser Asp Gly Ser Glu			
	230	235	240
cac aac tac acc tat tct tct gcg tgg ttc gat gtc atc agc cct gag			883
His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp Val Ile Ser Pro Glu			
	250	255	260
cca aag ctt ggc cgc tcc acc atc tcc cgt ggt tcc ctg gca aca ctt			931
Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly Ser Leu Ala Thr Leu			
	265	270	275
gct cag ctg gaa gaa ttg gca cca aag ctg gcc aag gat cca ctg aag			979
Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala Lys Asp Pro Leu Lys			
	280	285	290
ttt aat gct cca cag ctg atg aag gtt cca gat atc ttc cca tcc tgg			1027
Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp Ile Phe Pro Ser Trp			
	295	300	305

act ttg aac aag ctg acc ctt tcc gca gtc ggt gtg gct tac tac gcc 1075
 Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr Ala
 310 315 320 325

 atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc tac 1123
 Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe Tyr
 330 335 340

 caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc aag 1171
 Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser Lys
 345 350 355

 ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag cct 1219
 Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu Pro
 360 365 370

 ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc gca 1267
 Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser Ala
 375 380 385

 ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg tcc 1315
 Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu Ser
 390 395 400 405

 tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc cca 1363
 Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg Pro
 410 415 420

 ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa ttc 1411
 Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu Phe
 425 430 435

 ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag aac 1459
 Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu Asn
 440 445 450

 ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga aat 1507
 Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg Asn
 455 460 465

 gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga ctt 1555
 Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg Leu
 470 475 480 485

 gag ctt tct taagaaaggg cttgaactaa aca 1587
 Glu Leu Ser

<210> 850

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 850

Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala
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His Gly Ala Leu Pro Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg
 20 25 30

Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile
 35 40 45
 Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro
 50 55 60
 Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr
 65 70 75 80
 Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro
 85 90 95
 Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val
 100 105 110
 Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr
 115 120 125
 Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly
 130 135 140
 Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly
 145 150 155 160
 Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala Asp Gly
 165 170 175
 Arg Ile Leu His Leu Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly
 180 185 190
 Asp Leu Phe Trp Ala Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile
 195 200 205
 Val Arg Ala Arg Ile Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile
 210 215 220
 Ala Asp Thr Asp Arg Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His
 225 230 235 240
 Ser Asp Gly Ser Glu His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp
 245 250 255
 Val Ile Ser Pro Glu Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly
 260 265 270
 Ser Leu Ala Thr Leu Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala
 275 280 285
 Lys Asp Pro Leu Lys Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp
 290 295 300
 Ile Phe Pro Ser Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly
 305 310 315 320
 Val Ala Tyr Tyr Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn
 325 330 335
 Leu Thr Gln Phe Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg
 340 345 350

Gly Tyr Gly Ser Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr
 355 360 365
 Glu Ala Val Glu Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser
 370 375 380
 Gly His Tyr Ser Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn
 385 390 395 400
 Arg Ala Pro Leu Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp
 405 410 415
 Phe Pro Ile Arg Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys
 420 425 430
 Arg Val Met Glu Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg
 435 440 445
 Thr Ser Ala Glu Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp
 450 455 460
 Leu Lys Thr Arg Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp
 465 470 475 480
 Met Ser Arg Arg Leu Glu Leu Ser
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<210> 851

<211> 563

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(540)

<223> FRXA00420

<400> 851

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gcc atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc	96
Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe	
20 25 30	
tac caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc	144
Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser	
35 40 45	
aag ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag	192
Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu	
50 55 60	
cct ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc	240
Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser	
65 70 75 80	
gca ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg	288
Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu	

85										90					95					
tcc	tac	cca	atg	cca	ggc	tgg	aac	gtc	tgc	ggt	gac	ttc	cct	atc	cgc	336				
Ser	Tyr	Pro	Met	Pro	Gly	Trp	Asn	Val	Cys	Val	Asp	Phe	Pro	Ile	Arg					
			100				105						110							
cca	ggt	ctg	gga	gct	ttc	ttg	gac	gat	ctg	gac	aag	cgc	gtc	atg	gaa	384				
Pro	Gly	Leu	Gly	Ala	Phe	Leu	Asp	Asp	Leu	Asp	Lys	Arg	Val	Met	Glu					
			115				120						125							
ttc	ggc	ggc	cgc	ctc	tac	ctg	gcc	aag	gaa	tcc	cgc	acc	tcc	gca	gag	432				
Phe	Gly	Gly	Arg	Leu	Tyr	Leu	Ala	Lys	Glu	Ser	Arg	Thr	Ser	Ala	Glu					
			130				135						140							
aac	ttc	cac	gcc	atg	tac	cca	ggt	atg	gaa	ggc	tgg	ttg	aag	act	cga	480				
Asn	Phe	His	Ala	Met	Tyr	Pro	Gly	Met	Glu	Gly	Trp	Leu	Lys	Thr	Arg					
			145				150						155			160				
aat	gag	atc	gac	cca	acc	gga	gtc	ttt	gca	tct	gac	atg	tcc	cgc	cga	528				
Asn	Glu	Ile	Asp	Pro	Thr	Gly	Val	Phe	Ala	Ser	Asp	Met	Ser	Arg	Arg					
			165				170						175							
ctt	gag	ctt	tct	taagaaaggg cttgaactaa aca										563						
Leu	Glu	Leu	Ser																	
			180																	

<210> 852

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 852

Trp	Thr	Leu	Asn	Lys	Leu	Thr	Leu	Ser	Ala	Val	Gly	Val	Ala	Tyr	Tyr
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Ala	Met	Gly	Ala	Pro	Ala	Lys	Asn	Gln	Val	Lys	Asn	Leu	Thr	Gln	Phe
			20					25					30		
Tyr	Gln	Pro	Leu	Asp	Leu	Ile	Gly	Glu	Trp	Asn	Arg	Gly	Tyr	Gly	Ser
		35					40					45			
Lys	Gly	Phe	Leu	Gln	Tyr	Gln	Phe	Val	Val	Pro	Thr	Glu	Ala	Val	Glu
	50					55					60				
Pro	Phe	Lys	Asp	Ile	Ile	Arg	Asp	Met	Gln	Lys	Ser	Gly	His	Tyr	Ser
	65				70					75					80
Ala	Leu	Asn	Val	Phe	Lys	Leu	Phe	Gly	Pro	Gly	Asn	Arg	Ala	Pro	Leu
				85					90					95	
Ser	Tyr	Pro	Met	Pro	Gly	Trp	Asn	Val	Cys	Val	Asp	Phe	Pro	Ile	Arg
		100						105					110		
Pro	Gly	Leu	Gly	Ala	Phe	Leu	Asp	Asp	Leu	Asp	Lys	Arg	Val	Met	Glu
		115					120					125			
Phe	Gly	Gly	Arg	Leu	Tyr	Leu	Ala	Lys	Glu	Ser	Arg	Thr	Ser	Ala	Glu
	130					135					140				
Asn	Phe	His	Ala	Met	Tyr	Pro	Gly	Met	Glu	Gly	Trp	Leu	Lys	Thr	Arg

145		150		155		160
Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg						
		165		170		175
Leu Glu Leu Ser						
		180				

<210> 853
 <211> 622
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(622)
 <223> FRXA00426

<400> 853
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ttcaccacct gaaaattttc gggggtaacc tttaaaggcg atg aac agt tct cac 115
 Met Asn Ser Ser His
 1 5

ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc 163
 Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro
 10 15 20

cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc 211
 Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr
 25 30 35

gct gag gta ctt acc acc cca gac cta gac atc att gtg gat gca gtc 259
 Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val
 40 45 50

cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc 307
 Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg
 55 60 65

ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa 355
 Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln
 70 75 80 85

aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac 403
 Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His
 90 95 100

tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc 451
 Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr
 105 110 115

ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct 499
 Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro
 120 125 130

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547
 Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro
 135 140 145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595
Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His
150 155 160 165

gtg gtc tcc atg gaa ctc ctc gtt gca 622
Val Val Ser Met Glu Leu Leu Val Ala
170

<210> 854

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 854

Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala
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His Gly Ala Leu Pro Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg
20 25 30

Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile
35 40 45

Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro
50 55 60

Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr
65 70 75 80

Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro
85 90 95

Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val
100 105 110

Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr
115 120 125

Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly
130 135 140

Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly
145 150 155 160

Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala
165 170

<210> 855

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> RXN00708

<400> 855

cgc agc aac ttg gag gcg gta aag att tcg ctt atc gac gaa gac gtc 835
 Arg Ser Asn Leu Glu Ala Val Lys Ile Ser Leu Ile Asp Glu Asp Val
 230 235 240 245

cag gcg att acc gct ttg gcg cgc aaa aac ggc cgg atc aaa gat caa 883
 Gln Ala Ile Thr Ala Leu Ala Arg Lys Asn Gly Arg Ile Lys Asp Gln
 250 255 260

gat cca gcc gtc tat gaa gaa ttc tagatagtt catcaagggtt ccg 930
 Asp Pro Ala Val Tyr Glu Glu Phe
 265

<210> 856

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 856

Met Thr Leu Ser Leu Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp
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Gly Ala Pro Gly Val Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr
 20 25 30

Arg Leu Ile Asp Thr Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly
 35 40 45

Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu Ile Val Thr
 50 55 60

Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly Arg Val Arg
 65 70 75 80

Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile Asp Leu Leu
 85 90 95

Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val Glu Ala Trp
 100 105 110

Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys His Ile Gly
 115 120 125

Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg Arg Glu Thr
 130 135 140

Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro Tyr Phe Pro
 145 150 155 160

Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile Ile Thr Glu
 165 170 175

Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu Glu Pro Leu
 180 185 190

Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly Glu Ile Ala
 195 200 205

Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro Arg Ser Thr
 210 215 220

Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys Ile Ser Leu
225 230 235 240

Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg Lys Asn Gly
245 250 255

Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
260 265

<210> 857

<211> 695

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (672)

<223> FRXA00708

<400> 857

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Thr Val Gly Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu	
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att gtt acc agt aag ctc cct ggc cgc ttc cat gct cgc gat cta gga	96
Ile Val Thr Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly	
20 25 30	
cgc gtc cgc att gag gaa agt cta tac cgc ctc aac tta gat tac atc	144
Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile	
35 40 45	
gat ctc ctc ttg att cac tgg cct aat ccc agc aag gat ctc tac gtc	192
Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val	
50 55 60	
gag gcg tgg gaa acg ctg att gaa gtc cgc gat gct ggc ctg gtc aag	240
Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys	
65 70 75 80	
cac atc gga gtg tct aac ttc ctt cca aat cac att gat cgc ctg cgc	288
His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg	
85 90 95	
cgc gaa acc ggt gaa ctg ccg gcc gtt aac cag atc gag ttg cac ccc	336
Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro	
100 105 110	
tat ttc ccg cag gtg gag cag gta gat ttc cac gat gag ctg ggc atc	384
Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile	
115 120 125	
att acc gag gcc tgg agc ccg ctc agc aac ggt cgc gga ctc gtc gaa	432
Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu	
130 135 140	
gag cca ttg ctc aag gaa atc ggc gag cgc tac ggg gtc ggc agc ggc	480
Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly	
145 150 155 160	

gaa atc gcc ctc gct tgg cat cac gcc agg gga atc gtt ccg att cca 528
 Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro
 165 170 175
 cgc tcc acc aac ccg gcc agg cag cgc agc aac ttg gag gcg gta aag 576
 Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys
 180 185 190
 att tcg ctt atc gac gaa gac gtc cag gcg att acc gct ttg gcg cgc 624
 Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg
 195 200 205
 aaa aac ggc cgg atc aaa gat caa gat cca gcc gtc tat gaa gaa ttc 672
 Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
 210 215 220
 tagatagtta catcaagggtt ccg 695

<210> 858

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 858

Thr Val Gly Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu
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 Ile Val Thr Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly
 20 25 30
 Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile
 35 40 45
 Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val
 50 55 60
 Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys
 65 70 75 80
 His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg
 85 90 95
 Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro
 100 105 110
 Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile
 115 120 125
 Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu
 130 135 140
 Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly
 145 150 155 160
 Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro
 165 170 175
 Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys
 180 185 190

Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg
 195 200 205
 Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
 210 215 220

<210> 859
 <211> 1038
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1015)
 <223> RXA02373

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 Met Ser Val Val Gly
 1 5
 acc ggc cta ttc ttt gga tcc ccg gag gaa gag cgg gat aag ttg atg 163
 Thr Gly Leu Phe Phe Gly Ser Pro Glu Glu Glu Arg Asp Lys Leu Met
 10 15 20
 caa tct ttg atg gat cag aag aat aag ctt tcg aag tct gaa ggt atc 211
 Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser Lys Ser Glu Gly Ile
 25 30 35
 cca ttg gtc acc ttg aat gat gga aaa acc att cct cag ctt ggt ttt 259
 Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile Pro Gln Leu Gly Phe
 40 45 50
 ggt gtg ttc aag gta gat ccc gat gaa gca gag cgc gta gtt acc gaa 307
 Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu Arg Val Val Thr Glu
 55 60 65
 gca ctt gag gta ggt tac cgc cac atc gat act gct gcg att tac ggc 355
 Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr Ala Ala Ile Tyr Gly
 70 75 80 85
 aat gag gaa ggt gtc ggc cga gct att gct aag tcc ggc att cct cgt 403
 Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys Ser Gly Ile Pro Arg
 90 95 100
 gaa gag ctg ttt att act acc aag ttg tgg aac gat cgc cac ctg gat 451
 Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn Asp Arg His Leu Asp
 105 110 115
 gta gaa gct gct ttt gag gag tct ctg cag aag ctg ggc ttg gat tat 499
 Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys Leu Gly Leu Asp Tyr
 120 125 130
 gta gat ctg tac ttg gtg cac tgg ccg gca ccg aag aac gat aat tat 547

Val	Asp	Leu	Tyr	Leu	Val	His	Trp	Pro	Ala	Pro	Lys	Asn	Asp	Asn	Tyr	
135						140					145					
gtt	gct	gca	tgg	aag	ggc	ttg	gaa	aag	ctc	ggg	gac	cgt	gct	cgt	tcc	595
Val	Ala	Ala	Trp	Lys	Gly	Leu	Glu	Lys	Leu	Gly	Asp	Arg	Ala	Arg	Ser	
150					155					160					165	
atc	ggg	gtg	tgc	aac	ttc	ctg	cca	gag	cac	cta	gaa	aag	ctg	ctg	gca	643
Ile	Gly	Val	Cys	Asn	Phe	Leu	Pro	Glu	His	Leu	Glu	Lys	Leu	Leu	Ala	
				170					175						180	
gag	gca	acc	act	gtg	cct	gcc	att	aac	cag	att	gag	ctg	cac	cca	gct	691
Glu	Ala	Thr	Thr	Val	Pro	Ala	Ile	Asn	Gln	Ile	Glu	Leu	His	Pro	Ala	
				185					190					195		
ttg	cag	cag	cgc	gat	gct	gtt	gag	gca	tct	ctt	gca	gca	ggc	atc	act	739
Leu	Gln	Gln	Arg	Asp	Ala	Val	Glu	Ala	Ser	Leu	Ala	Ala	Gly	Ile	Thr	
		200					205					210				
gtg	gag	tgc	tgg	ggg	cct	ctg	gga	cag	ggg	cgt	ttt	gat	ctt	ggc	gct	787
Val	Glu	Ser	Trp	Gly	Pro	Leu	Gly	Gln	Gly	Arg	Phe	Asp	Leu	Gly	Ala	
	215					220					225					
gag	gaa	cca	atc	gca	gct	gca	gcg	aag	aac	cat	gga	aag	acc	cca	gct	835
Glu	Glu	Pro	Ile	Ala	Ala	Ala	Ala	Lys	Asn	His	Gly	Lys	Thr	Pro	Ala	
230					235					240					245	
cag	gtt	gtt	atc	cgt	tgg	cac	ctg	cag	aac	ggg	ttc	gtt	gtg	ttc	ccc	883
Gln	Val	Val	Ile	Arg	Trp	His	Leu	Gln	Asn	Gly	Phe	Val	Val	Phe	Pro	
				250					255					260		
aag	act	gtg	act	aag	agc	cgc	atg	gtg	gaa	aac	atc	gac	gtg	ttt	gat	931
Lys	Thr	Val	Thr	Lys	Ser	Arg	Met	Val	Glu	Asn	Ile	Asp	Val	Phe	Asp	
				265				270					275			
ttc	gaa	ctc	agt	gat	gag	gag	atg	gct	gcg	atc	act	gct	ctt	gag	cgc	979
Phe	Glu	Leu	Ser	Asp	Glu	Glu	Met	Ala	Ala	Ile	Thr	Ala	Leu	Glu	Arg	
		280					285					290				
aat	gat	cgt	ggg	ggg	tca	cac	ccg	aat	gat	ctg	aac	tagaaataag				1025
Asn	Asp	Arg	Gly	Gly	Ser	His	Pro	Asn	Asp	Leu	Asn					
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<210> 860

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 860

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			20					25					30			
Lys	Ser	Glu	Gly	Ile	Pro	Leu	Val	Thr	Leu	Asn	Asp	Gly	Lys	Thr	Ile	
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Pro Gln Leu Gly Phe Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu
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Arg Val Val Thr Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr
  65                      70                      75                      80

Ala Ala Ile Tyr Gly Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys
                      85                      90                      95

Ser Gly Ile Pro Arg Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn
      100                      105                      110

Asp Arg His Leu Asp Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys
      115                      120                      125

Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro
      130                      135                      140

Lys Asn Asp Asn Tyr Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly
      145                      150                      155                      160

Asp Arg Ala Arg Ser Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu
      165                      170                      175

Glu Lys Leu Leu Ala Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile
      180                      185                      190

Glu Leu His Pro Ala Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu
      195                      200                      205

Ala Ala Gly Ile Thr Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg
      210                      215                      220

Phe Asp Leu Gly Ala Glu Glu Pro Ile Ala Ala Ala Lys Asn His
      225                      230                      235                      240

Gly Lys Thr Pro Ala Gln Val Val Ile Arg Trp His Leu Gln Asn Gly
      245                      250                      255

Phe Val Val Phe Pro Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn
      260                      265                      270

Ile Asp Val Phe Asp Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile
      275                      280                      285

Thr Ala Leu Glu Arg Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu
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Asn
305

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<210> 861

<211> 1683

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1660)

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               Met Ile Thr Ala Thr
               1 5

gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163
Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
               10 15 20

aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211
Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
               25 30 35

cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259
Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu Arg Ala Ala Thr Thr
               40 45 50

tcg gcg aag cga gct ttt gaa agc tac cga ctc act act cca gag gtt 307
Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu Thr Thr Pro Glu Val
               55 60 65

aga gca gat ttc ctg gat tcc atc gct gac aac atc gat gcg cta tcc 355
Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn Ile Asp Ala Leu Ser
               70 75 80 85

ggc gag atc gtg caa cgg gcg agc ctg gag aca ggt ttg gga act acc 403
Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr Gly Leu Gly Thr Thr
               90 95 100

cga ctc aca ggc gaa gta gcc cgc acc agc aac cag ctc cgc ctg ttt 451
Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn Gln Leu Arg Leu Phe
               105 110 115

gca gaa acc gtg aga agc gga cag ttc cac cga gta cgc att gaa cga 499
Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg Val Arg Ile Glu Arg
               120 125 130

gga ccg cgg att gat ctt cgc cag cgt cag gtt ccg ttg gga cca gtc 547
Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val Pro Leu Gly Pro Val
               135 140 145

gcg gta ttc ggg gca agc aac ttc ccc gtc gct ttc tct act gct ggt 595
Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala Phe Ser Thr Ala Gly
               150 155 160 165

ggc gat aca gca tca gcg ttg gct gca ggc tgc cct gtg gtt ttt aag 643
Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys Pro Val Val Phe Lys
               170 175 180

gcg cat aat gcg cac cct gga aca gct gag ctc gtc ggg caa gcg gtg 691
Ala His Asn Ala His Pro Gly Thr Ala Glu Leu Val Gly Gln Ala Val
               185 190 195

cgg gga gcc gtc gaa aag cat gag ttt gat gct ggt gtg ttt aac ctt 739
Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala Gly Val Phe Asn Leu
               200 205 210

gtc tac ggc cgt ggc gtg gaa att ggc cag gag ctg gct gcg gat ccg 787

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Val	Tyr	Gly	Arg	Gly	Val	Glu	Ile	Gly	Gln	Glu	Leu	Ala	Ala	Asp	Pro	
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Asn	Ile	Thr	Ala	Ile	Gly	Phe	Thr	Gly	Ser	Arg	Gln	Gly	Gly	Leu	Ala	
230					235					240					245	
ctg	tca	cag	act	gcg	ttt	agc	cgc	cca	gtt	ccc	gtt	cca	gtc	ttt	gca	883
Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala	
				250					255					260		
gaa	atg	agt	gcc	acc	aac	cct	gtg	ttc	gtc	ttc	ccc	ggc	gcg	ctg	gcg	931
Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala	
			265				270					275				
gat	ttg	gat	gca	tcg	agt	tcc	ttg	gct	gag	gcg	ttt	acc	gct	tcc	gtc	979
Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val	
			280				285					290				
acc	ggc	agt	tcc	ggg	caa	ttg	tgc	acc	aag	cct	ggc	ctc	gtt	ttc	atc	1027
Thr	Gly	Ser	Ser	Gly	Gln	Leu	Cys	Thr	Lys	Pro	Gly	Leu	Val	Phe	Ile	
	295				300						305					
ccg	cgc	ggg	gtt	gtt	ggg	gat	gct	ttt	gtg	gcg	ctc	gta	gca	gcc	aaa	1075
Pro	Arg	Gly	Val	Val	Gly	Asp	Ala	Phe	Val	Ala	Leu	Val	Ala	Ala	Lys	
310					315					320					325	
ttt	aaa	gaa	acc	acg	ggg	caa	acg	atg	ctc	acg	caa	ggc	atc	gct	cag	1123
Phe	Lys	Glu	Thr	Thr	Gly	Gln	Thr	Met	Leu	Thr	Gln	Gly	Ile	Ala	Gln	
				330					335					340		
gca	tgg	cag	cgc	gga	gtc	gac	aac	ctt	gca	gca	cag	cca	agt	gta	aaa	1171
Ala	Trp	Gln	Arg	Gly	Val	Asp	Asn	Leu	Ala	Ala	Gln	Pro	Ser	Val	Lys	
			345				350						355			
atc	ctc	gcc	caa	ggc	acc	ccc	gga	gat	gga	gag	aac	gcg	ccg	ggc	ccg	1219
Ile	Leu	Ala	Gln	Gly	Thr	Pro	Gly	Asp	Gly	Glu	Asn	Ala	Pro	Gly	Pro	
		360					365					370				
gtg	gtg	ttt	gaa	agt	gat	gtg	cag	gcg	ttg	cta	aat	aat	gtg	gtg	ttg	1267
Val	Val	Phe	Glu	Ser	Asp	Val	Gln	Ala	Leu	Leu	Asn	Asn	Val	Val	Leu	
	375					380					385					
cag	gaa	gaa	atc	ttc	ggg	gcg	gca	tcg	ctg	gtg	gtg	cgt	tat	gat	tcc	1315
Gln	Glu	Glu	Ile	Phe	Gly	Ala	Ala	Ser	Leu	Val	Val	Arg	Tyr	Asp	Ser	
390					395					400					405	
ccg	gat	caa	ctc	cac	caa	gta	gcc	aat	tca	ctc	gag	gga	caa	tta	aca	1363
Pro	Asp	Gln	Leu	His	Gln	Val	Ala	Asn	Ser	Leu	Glu	Gly	Gln	Leu	Thr	
				410					415					420		
gcc	acg	atc	cac	gca	tcc	cag	gat	gat	ttc	cag	gaa	gtc	tcg	aaa	ctt	1411
Ala	Thr	Ile	His	Ala	Ser	Gln	Asp	Asp	Phe	Gln	Glu	Val	Ser	Lys	Leu	
			425				430						435			
atc	ccc	ctc	ttg	gag	gat	ctc	gcg	ggc	cgt	gtt	ctt	tac	ggc	ggc	tgg	1459
Ile	Pro	Leu	Leu	Glu	Asp	Leu	Ala	Gly	Arg	Val	Leu	Tyr	Gly	Gly	Trp	
		440				445						450				
cca	acg	ggg	gtg	gaa	gtt	ggg	cac	acg	gtt	atc	cat	gga	ggc	cct	tat	1507
Pro	Thr	Gly	Val	Glu	Val	Gly	His	Thr	Val	Ile	His	Gly	Gly	Pro	Tyr	

455	460	465	
ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc			1555
Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile			
470	475	480	485
gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg			1603
Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu			
	490	495	500
ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa			1651
Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu			
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ata gac cgt taatagctgg tctttacatt tgc			1683
Ile Asp Arg			
	520		
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<212> PRT			
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<400> 862			
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Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu			
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Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu			
	50	55	60
Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn			
	65	70	75
Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr			
	85	90	95
Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn			
	100	105	110
Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg			
	115	120	125
Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val			
	130	135	140
Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala			
	145	150	155
Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys			
	165	170	175
Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu			
	180	185	190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
 195 200 205
 Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
 210 215 220
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
 225 230 235 240
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
 245 250 255
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
 260 265 270
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
 275 280 285
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
 290 295 300
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala
 305 310 315 320
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr
 325 330 335
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala
 340 345 350
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu
 355 360 365
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu
 370 375 380
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val
 385 390 395 400
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu
 405 410 415
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln
 420 425 430
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val
 435 440 445
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile
 450 455 460
 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val
 465 470 475 480
 Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr
 485 490 495
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515

520

<210> 863

<211> 882

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXS00419

<400> 863

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 Met Leu Asn Ala Val
 1 5

ggc aaa gcc caa aac att ctc ctt ctt ggt gga acc tct gag atc ggt 163
 Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly Thr Ser Glu Ile Gly
 10 15 20

att tcc att gtc tcc cgc ttc ctc aag cag ggt cca tcc cat gtg acc 211
 Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly Pro Ser His Val Thr
 25 30 35

ttg gca gcg cgt aaa gat tcc cca cgc gtg gac gca gca gtc gca gag 259
 Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp Ala Ala Val Ala Glu
 40 45 50

atc aaa gca gct ggc gct gct tcc gtt gct gtt gtt gat ttc gat gcg 307
 Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val Val Asp Phe Asp Ala
 55 60 65

ctc gac acc gaa tcc cac cct gca gcc atc gac gca gcc ttt gaa aac 355
 Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp Ala Ala Phe Glu Asn
 70 75 80 85

ggc gac gtt gac gta gca atc gtg gct ttc ggc atc ctc ggc gac aac 403
 Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly Ile Leu Gly Asp Asn
 90 95 100

gaa gca cag tgg cgc gac caa gca cta gca gtg gaa gca acc acc gtg 451
 Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val Glu Ala Thr Thr Val
 105 110 115

aac tac acc gcc ggc gtt tcc gta ggt gta ctg ctg ggc cag aaa ttt 499
 Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu Leu Gly Gln Lys Phe
 120 125 130

gag cag cag ggc cac ggc acc atc gtg gca ttg tcc tct gtg gca ggc 547
 Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu Ser Ser Val Ala Gly
 135 140 145

cag cga gtc cgc cgc tcc aac ttt gtc tac ggc tcc gcc aag gca ggt 595
 Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly Ser Ala Lys Ala Gly
 150 155 160 165

ttc gac ggt ttc tac acc cag ctc ggc gaa gcc ctg cgt gga tcc ggt 643

Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly Ser Gly
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 gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag atg tcc 691
 Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys Met Ser
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 gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac gtg gca 739
 Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp Val Ala
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 gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc ttt gtc 787
 Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile Phe Val
 215 220 225
 cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att ccg cga 835
 His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile Pro Arg
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 Ala Ile Phe Arg Lys Leu Pro Phe
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<210> 864

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 864

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 Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp
 35 40 45
 Ala Ala Val Ala Glu Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val
 50 55 60
 Val Asp Phe Asp Ala Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp
 65 70 75 80
 Ala Ala Phe Glu Asn Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly
 85 90 95
 Ile Leu Gly Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val
 100 105 110
 Glu Ala Thr Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu
 115 120 125
 Leu Gly Gln Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu
 130 135 140
 Ser Ser Val Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly
 145 150 155 160
 Ser Ala Lys Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala

165								170				175					
Leu	Arg	Gly	Ser	Gly	Ala	Asn	Val	Leu	Val	Val	Arg	Pro	Gly	Gln	Val		
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Arg	Thr	Lys	Met	Ser	Ala	Asp	Gly	Gly	Glu	Ala	Pro	Leu	Thr	Val	Asn		
195								200				205					
Arg	Glu	Asp	Val	Ala	Asp	Ala	Val	Tyr	Asp	Ala	Val	Val	Asn	Lys	Lys		
210								215				220					
Asp	Ile	Ile	Phe	Val	His	Pro	Leu	Phe	Gln	Tyr	Val	Ser	Phe	Ala	Phe		
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Gln	Phe	Ile	Pro	Arg	Ala	Ile	Phe	Arg	Lys	Leu	Pro	Phe					
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<210> 865

<211> 1673

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1) .. (1650)

<223> RXC00416

<400> 865

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1				5				10						15		
att	ccg	ctg	tct	gcg	acc	cgc	ctg	tat	ttg	gac	gga	atc	agc	ggt	gac	96
Ile	Pro	Leu	Ser	Ala	Thr	Arg	Leu	Tyr	Leu	Asp	Gly	Ile	Ser	Val	Asp	
			20				25					30				
cag	ggc	ttt	aga	act	cag	ttt	tta	acc	cgc	atg	gct	gac	gat	atc	ggc	144
Gln	Gly	Phe	Arg	Thr	Gln	Phe	Leu	Thr	Arg	Met	Ala	Asp	Asp	Ile	Gly	
		35				40					45					
ttg	tcg	gac	atg	aac	tac	atc	gat	atg	cct	acc	ttc	tac	cct	gct	gga	192
Leu	Ser	Asp	Met	Asn	Tyr		Ile	Asp	Met	Pro	Thr	Phe	Tyr	Pro	Ala	Gly
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tgg	ttc	tgg	ctc	ggt	ggt	cgc	ttg	gcc	aat	ctt	ttg	ggg	ctg	ccc	ggt	240
Trp	Phe	Trp	Leu	Gly	Gly	Arg	Leu	Ala	Asn	Leu	Leu	Gly	Leu	Pro	Gly	
65				70			75							80		
tgg	gaa	gct	ttc	cag	cca	tgg	gca	att	gtg	tcc	atg	gca	ggt	gct	gct	288
Trp	Glu	Ala	Phe	Gln	Pro	Trp	Ala	Ile	Val	Ser	Met	Ala	Val	Ala	Ala	
				85			90							95		
tct	gtg	tta	ggt	cca	gtg	tgg	cag	cgc	atc	acc	ggt	tcc	ctg	ccg	gtg	336
Ser	Val	Leu	Val	Pro	Val	Trp	Gln	Arg	Ile	Thr	Gly	Ser	Leu	Pro	Val	
		100					105						110			
gca	aca	ggc	att	gcg	ttg	gtg	aca	acc	tgc	att	atc	ttg	gcg	atg	aat	384
Ala	Thr	Gly	Ile	Ala	Leu	Val	Thr	Thr	Cys	Ile	Ile	Leu	Ala	Met	Asn	
		115					120					125				

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Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met	
130 135 140	
ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc	480
Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala	
145 150 155 160	
ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc	528
Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe	
165 170 175	
acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg	576
Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala	
180 185 190	
gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg	624
Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu	
195 200 205	
ggg ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt	672
Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu	
210 215 220	
ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac	720
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His	
225 230 235 240	
tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca	768
Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser	
245 250 255	
agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg	816
Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val	
260 265 270	
cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg	864
Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val	
275 280 285	
ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac	912
Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn	
290 295 300	
acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc	960
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala	
305 310 315 320	
acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat	1008
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr	
325 330 335	
cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc	1056
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr	
340 345 350	
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Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln	
355 360 365	
gat ctg ccg cag aag aac gca cga gct atc gat ctg gcc tat acc gat	1152

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370						375					380					
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Thr	Asp	Gly	Tyr	Gly	Glu	Arg	Ala	Asp	Leu	Tyr	Pro	Ala	Gly	Ala	Ala	
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cgt	tat	tac	aag	gac	atc	aac	gat	cat	ctg	ctt	gat	caa	gga	ttc	gag	1248
Arg	Tyr	Tyr	Lys	Asp	Ile	Asn	Asp	His	Leu	Leu	Asp	Gln	Gly	Phe	Glu	
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cct	tcc	gaa	act	gtc	gtg	ctg	aca	gac	gaa	ctc	gat	ttc	atg	tcc	tac	1296
Pro	Ser	Glu	Thr	Val	Val	Leu	Thr	Asp	Glu	Leu	Asp	Phe	Met	Ser	Tyr	
			420					425					430			
tac	cct	tat	cgc	gga	tac	caa	gct	ttt	act	tcc	cac	tac	gcc	aac	ccg	1344
Tyr	Pro	Tyr	Arg	Gly	Tyr	Gln	Ala	Phe	Thr	Ser	His	Tyr	Ala	Asn	Pro	
			435				440					445				
ctt	ggt	gag	ttc	gga	aac	agg	aac	gca	ttc	atc	gaa	gat	ctc	gcg	atc	1392
Leu	Gly	Glu	Phe	Gly	Asn	Arg	Asn	Ala	Phe	Ile	Glu	Asp	Leu	Ala	Ile	
	450					455					460					
cga	agc	tgg	gat	gag	ttg	gct	gat	cct	caa	caa	ttc	agc	gac	gcc	ttg	1440
Arg	Ser	Trp	Asp	Glu	Leu	Ala	Asp	Pro	Gln	Gln	Phe	Ser	Asp	Ala	Leu	
	465				470					475					480	
aac	acc	tct	cca	tgg	acg	atc	cct	gag	gtg	ttc	atc	ttc	cgt	ggc	tcc	1488
Asn	Thr	Ser	Pro	Trp	Thr	Ile	Pro	Glu	Val	Phe	Ile	Phe	Arg	Gly	Ser	
				485					490					495		
atc	gat	gat	cct	gac	gcc	ggt	tgg	aaa	tac	gac	gtg	gct	gaa	gat	ctg	1536
Ile	Asp	Asp	Pro	Asp	Ala	Gly	Trp	Lys	Tyr	Asp	Val	Ala	Glu	Asp	Leu	
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Tyr	Pro	Asn	Asn	Pro	Asn	Val	Arg	Phe	Arg	Gly	Val	Tyr	Phe	Asn	Pro	
		515					520					525				
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Glu	Ser	Phe	Asp	Gln	Met	Trp	Gln	Thr	Lys	Gln	Val	Gly	Pro	Phe	Val	
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gtg	gta	acg	cac	aat	gag	taattcctca	ccaaacgacc	caa								1673
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	545				550											

<210> 866

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 866

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		20						25					30		

Gln	Gly	Phe	Arg	Thr	Gln	Phe	Leu	Thr	Arg	Met	Ala	Asp	Asp	Ile	Gly
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35					40					45					
Leu	Ser	Asp	Met	Asn	Tyr	Ile	Asp	Met	Pro	Thr	Phe	Tyr	Pro	Ala	Gly
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Trp	Phe	Trp	Leu	Gly	Gly	Arg	Leu	Ala	Asn	Leu	Leu	Gly	Leu	Pro	Gly
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Trp	Glu	Ala	Phe	Gln	Pro	Trp	Ala	Ile	Val	Ser	Met	Ala	Val	Ala	Ala
				85		90					95				
Ser	Val	Leu	Val	Pro	Val	Trp	Gln	Arg	Ile	Thr	Gly	Ser	Leu	Pro	Val
				100		105					110				
Ala	Thr	Gly	Ile	Ala	Leu	Val	Thr	Thr	Cys	Ile	Ile	Leu	Ala	Met	Asn
115			120					125							
Ser	Glu	Glu	Pro	Tyr	Ala	Ala	Ile	Val	Ala	Met	Gly	Ile	Pro	Ala	Met
130		135					140								
Leu	Val	Leu	Ala	Ser	Arg	Ile	Ala	Lys	Gly	Asp	Lys	Phe	Ala	Leu	Ala
145		150					155					160			
Gly	Gly	Ile	Ile	Tyr	Leu	Gly	Val	Ser	Ala	Thr	Phe	Tyr	Thr	Leu	Phe
				165		170					175				
Thr	Gly	Ala	Ile	Ala	Leu	Ser	Ala	Val	Ala	Val	Cys	Ile	Val	Val	Ala
				180		185					190				
Ala	Ile	Val	Gln	Arg	Ser	Ile	Lys	Pro	Leu	Leu	Trp	Leu	Ala	Val	Leu
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210		215					220								
Leu	Ala	Ser	Ile	Asn	Gly	Ala	Glu	Arg	Ser	Gly	Asp	Ser	Ala	Thr	His
225		230					235					240			
Tyr	Leu	Pro	Leu	Glu	Gly	Thr	Gln	Phe	Pro	Val	Pro	Phe	Leu	Ala	Ser
				245		250					255				
Ser	Val	Val	Gly	Leu	Leu	Cys	Leu	Val	Gly	Leu	Ile	Tyr	Leu	Val	Val
			260		265					270					
Arg	Phe	His	Asn	Asn	Glu	Val	Arg	Ala	Met	Trp	Val	Gly	Ile	Ala	Val
275			280					285							
Phe	Tyr	Ala	Trp	Met	Gly	Met	Ser	Met	Ala	Ile	Thr	Leu	Leu	Gly	Asn
290		295					300								
Thr	Leu	Leu	Gly	Phe	Arg	Leu	Asp	Thr	Val	Leu	Val	Leu	Ile	Phe	Ala
305		310					315					320			
Thr	Ala	Gly	Val	Leu	Gly	Ile	Ala	Asp	Phe	Arg	Leu	Ala	Ser	Val	Tyr
				325		330					335				
Gln	Leu	Tyr	Pro	Thr	Gln	Ile	Thr	Glu	Arg	Thr	Ala	Thr	His	Leu	Thr
340				345					350						
Asn	Leu	Ile	Val	Val	Leu	Val	Leu	Leu	Gly	Gly	Leu	Tyr	Tyr	Ala	Gln
355		360					365								

Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
 370 375 380
 Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
 385 390 395 400
 Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
 405 410 415
 Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
 420 425 430
 Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
 435 440 445
 Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
 450 455 460
 Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
 465 470 475 480
 Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
 485 490 495
 Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
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 Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
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 Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
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 Val Val Thr His Asn Glu
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<210> 867

<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> RXC02206

<400> 867

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 Met Val Gly Ser Ser
 1 5
 ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163
 Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
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 ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211
 Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn

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Ser	Gly	Gly	Thr	Leu	Ile	Asp	Val	Ser	Pro	Asn	Tyr	Thr	Thr	Gly	Val			
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gcg	gaa	gaa	atg	ctc	ggc	acg	atg	ttg	gat	gcg	gaa	gtc	tct	cgt	tcg	307		
Ala	Glu	Glu	Met	Leu	Gly	Thr	Met	Leu	Asp	Ala	Glu	Val	Ser	Arg	Ser			
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gct	gtc	gtc	att	tcc	tcc	agc	gca	ggg	gtc	aac	ccc	gct	ctg	ccg	ctc	355		
Ala	Val	Val	Ile	Ser	Ser	Ser	Ala	Gly	Val	Asn	Pro	Ala	Leu	Pro	Leu			
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ggc	cga	cgt	gtg	gat	tgc	tcc	cgc	cgc	aat	ttg	att	gcc	caa	tta	gat	403		
Gly	Arg	Arg	Val	Asp	Cys	Ser	Arg	Arg	Asn	Leu	Ile	Ala	Gln	Leu	Asp			
				90					95					100				
gtc	acc	ctg	cgg	gca	tta	aac	act	gac	tat	ttg	gat	ttg	tgg	tct	gtg	451		
Val	Thr	Leu	Arg	Ala	Leu	Asn	Thr	Asp	Tyr	Leu	Asp	Leu	Trp	Ser	Val			
			105					110					115					
ggc	tat	tgg	gat	gag	ggc	acc	cca	ccg	cat	gag	gtg	gcc	gat	act	ttg	499		
Gly	Tyr	Trp	Asp	Glu	Gly	Thr	Pro	Pro	His	Glu	Val	Ala	Asp	Thr	Leu			
		120					125					130						
gat	tac	gcc	gtg	cgc	acc	ggc	cga	gtc	cga	tat	gcc	ggg	gtc	cga	gga	547		
Asp	Tyr	Ala	Val	Arg	Thr	Gly	Arg	Val	Arg	Tyr	Ala	Gly	Val	Arg	Gly			
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Tyr	Ser	Gly	Trp	Gln	Leu	Ala	Val	Thr	His	Ala	Ala	Ser	Asn	His	Ala			
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gcg	gcc	tcc	gcc	cgc	ccc	gtg	gtc	gtt	gca	caa	aat	gaa	tac	agc	ctg	643		
Ala	Ala	Ser	Ala	Arg	Pro	Val	Val	Val	Ala	Gln	Asn	Glu	Tyr	Ser	Leu			
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ctg	gaa	cgc	cgc	gca	gaa	caa	gaa	ctc	ctc	cct	gcc	acc	caa	cac	cta	691		
Leu	Glu	Arg	Arg	Ala	Glu	Gln	Glu	Leu	Leu	Pro	Ala	Thr	Gln	His	Leu			
			185					190					195					
ggg	gtc	gga	ttc	ttt	gct	ggc	gct	ccg	ctg	ggg	caa	ggc	gtg	ctg	act	739		
Gly	Val	Gly	Phe	Phe	Ala	Gly	Ala	Pro	Leu	Gly	Gln	Gly	Val	Leu	Thr			
		200				205						210						
gct	aaa	tac	cgc	tcc	gaa	att	ccc	cat	gat	tcc	aga	gct	gca	tcc	aca	787		
Ala	Lys	Tyr	Arg	Ser	Glu	Ile	Pro	His	Asp	Ser	Arg	Ala	Ala	Ser	Thr			
	215					220					225							
gga	cgc	gac	gca	gaa	gtc	caa	agc	tac	cta	gat	aat	cga	ggc	cgc	atc	835		
Gly	Arg	Asp	Ala	Glu	Val	Gln	Ser	Tyr	Leu	Asp	Asn	Arg	Gly	Arg	Ile			
	230				235					240					245			
att	gtc	gat	gct	ctt	gat	act	gca	gcc	aaa	gga	tta	ggc	att	agc	ccc	883		
Ile	Val	Asp	Ala	Leu	Asp	Thr	Ala	Ala	Lys	Gly	Leu	Gly	Ile	Ser	Pro			
				250					255						260			
gct	gtc	acag	gcc	acc	acc	tgg	gtg	cgt	gat	cgt	ccc	gga	gtg	aca	gct	931		
Ala	Val	Thr	Ala	Thr	Thr	Trp	Val	Arg	Asp	Arg	Pro	Gly	Val	Thr	Ala			
			265					270					275					

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<210> 868
<211> 312
<212> PRT
<213> Corynebacterium glutamicum
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<400> 868															
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Ser	Thr	Trp	Gly 20	Ser	Gly	Thr	Glu	Leu 25	Ala	Glu	Ala	Gly	Asp 30	Ile	Phe
Lys	Ala	Phe 35	Ile	Asn	Ser	Gly	Gly 40	Thr	Leu	Ile	Asp	Val 45	Ser	Pro	Asn
Tyr	Thr 50	Thr	Gly	Val	Ala	Glu 55	Glu	Met	Leu	Gly	Thr 60	Met	Leu	Asp	Ala
Glu 65	Val	Ser	Arg	Ser	Ala 70	Val	Val	Ile	Ser	Ser 75	Ser	Ala	Gly	Val	Asn 80
Pro	Ala	Leu	Pro	Leu 85	Gly	Arg	Arg	Val	Asp 90	Cys	Ser	Arg	Arg	Asn 95	Leu
Ile	Ala	Gln	Leu 100	Asp	Val	Thr	Leu	Arg 105	Ala	Leu	Asn	Thr 110	Asp	Tyr	Leu
Asp	Leu 115	Trp	Ser	Val	Gly	Tyr	Trp 120	Asp	Glu	Gly	Thr 125	Pro	Pro	His	Glu
Val 130	Ala	Asp	Thr	Leu	Asp	Tyr 135	Ala	Val	Arg	Thr	Gly 140	Arg	Val	Arg	Tyr
Ala 145	Gly	Val	Arg	Gly	Tyr 150	Ser	Gly	Trp	Gln	Leu 155	Ala	Val	Thr	His	Ala 160
Ala	Ser	Asn	His	Ala 165	Ala	Ala	Ser	Ala	Arg 170	Pro	Val	Val	Val	Ala 175	Gln
Asn	Glu	Tyr	Ser 180	Leu	Leu	Glu	Arg	Arg 185	Ala	Glu	Gln	Glu	Leu 190	Leu	Pro
Ala	Thr 195	Gln	His	Leu	Gly	Val	Gly 200	Phe	Phe	Ala	Gly	Ala 205	Pro	Leu	Gly
Gln 210	Gly	Val	Leu	Thr	Ala	Lys 215	Tyr	Arg	Ser	Glu	Ile 220	Pro	His	Asp	Ser

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
 225 230 235 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
 245 250 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
 260 265 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
 275 280 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
 290 295 300

Gln Ala Leu Asp Asp Val Ser Leu
 305 310

<210> 869
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(598)
 <223> RXS03074

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 tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
 Met Thr Gln Ser Ala
 1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

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att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
      105                      110                      115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
      120                      125                      130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
      135                      140                      145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
150                      155                      160                      165

cag taatttgttt tgacgacgca gta 621
Gln

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<210> 870
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

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<400> 870
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Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
      20              25              30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
      35              40              45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
      50              55              60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
      65              70              75              80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
      85              90              95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
      100              105              110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
      115              120              125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
      130              135              140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
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Glu Ala Pro Ile Lys Gln
      165

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<210> 871
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 <212> DNA
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<220>
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 <223> FRXA02906

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 tagcaggaca agcataactgt ttttagttcta tgctgtgggc atg act caa agt gct 115
 Met Thr Gln Ser Ala
 1 5
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35
 ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165
 cag taatttggttt tgacgacgca gta 621
 Gln

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<400> 873
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gaatcgtatc cgtacctgga gacgatctag actgttctgc atg tcc agc acg cca 115
                                         Met Ser Ser Thr Pro
                                         1                               5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
                        10                        15                        20

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act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tgc ctt	211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu	
25 30 35	
gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag	259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu	
40 45 50	
cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg	307
Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg	
55 60 65	
ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg	355
Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu	
70 75 80 85	
cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc	403
Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu	
90 95 100	
tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg	451
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr	
105 110 115	
att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc	499
Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile	
120 125 130	
act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg	547
Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu Ser Leu Ala Gln Gly	
135 140 145	
gct tcc cag att ccg cgt cat ttc aat ctt gca ctt gat gtt cct ttg	595
Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala Leu Asp Val Pro Leu	
150 155 160 165	
gtt gct cct gaa ctg cca gag ctt cat ggt gag gca gtt gga gca tca	643
Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu Ala Val Gly Ala Ser	
170 175 180	
tgg acg cat cgc tgg atc aac cac ggt gag gtg acc gtg gac ctg ggg	691
Trp Thr His Arg Trp Ile Asn His Gly Glu Val Thr Val Asp Leu Gly	
185 190 195	
gag cac acc ctc gtg att gcc ggt gat gaa gca tgg gaa gtg gaa ggg	739
Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala Trp Glu Val Glu Gly	
200 205 210	
ctg gaa gat gtg ccc acc atc gct gaa cct act gca cca aag cct tat	787
Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr Ala Pro Lys Pro Tyr	
215 220 225	
aat ccg gtg cac cca ctg gct gct gaa atc ttg ctg aag gag cag gtc	835
Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu Leu Lys Glu Gln Val	
230 235 240 245	
tcc gcg gaa ggc tat gtg gta aac acc agg cct gat cat gtg atc gtg	883
Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro Asp His Val Ile Val	
250 255 260	

gtg gga cac ccc acg ctg cac cgc gga gtg ttg aag ttg atg tca gat	931
Val Gly His Pro Thr Leu His Arg Gly Val Leu Lys Leu Met Ser Asp	
265 270 275	
cct ggc att aaa tta act gtg ctt tca cgc acc gat atc atc act gat	979
Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr Asp Ile Ile Thr Asp	
280 285 290	
ccc ggc cgc cat gcc gat cag gtg ggc agc aca gtg aaa gtc acc ggc	1027
Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr Val Lys Val Thr Gly	
295 300 305	
acc cag gaa aag cag tgg cta aag atc tgt tgc gca gca tca gaa ctt	1075
Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser Ala Ala Ser Glu Leu	
310 315 320 325	
gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc	1123
Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn Gln Glu Phe Gly Phe	
330 335 340	
acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc	1171
Thr Gly Leu His Val Ala Ala Val Ala Asp Thr Leu Gly Thr Gly	
345 350 355	
gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg	1219
Asp Thr Leu Phe Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu	
360 365 370	
gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc	1267
Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val	
375 380 385	
gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct	1315
Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala	
390 395 400 405	
gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc	1363
Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala	
410 415 420	
ctt ctg ggc gat ctg tgc ttc ctt cac gat att ggc gga ctg ctc atc	1411
Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile	
425 430 435	
ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac	1459
Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn	
440 445 450	
gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt	1507
Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly	
455 460 465	
ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc	1555
Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser	
470 475 480 485	
atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac	1603
Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp	
490 495 500	
aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc	1651

Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser
 505 510 515

gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca 1699
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala
 520 525 530

caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt 1749
 Gln Gln Gln Ala Leu Met Asp Thr Val His
 535 540

gcg 1752

<210> 874

<211> 543

<212> PRT

<213> Corynebacterium glutamicum

<400> 874

Met Ser Ser Thr Pro Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser
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Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
 20 25 30

Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
 35 40 45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
 50 55 60

Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
 65 70 75 80

Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
 85 90 95

Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
 100 105 110

Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
 115 120 125

Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
 130 135 140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
 145 150 155 160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
 165 170 175

Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
 180 185 190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
 195 200 205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
 210 215 220

Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
 225 230 235 240
 Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
 245 250 255
 Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
 260 265 270
 Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
 275 280 285
 Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
 290 295 300
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
 305 310 315 320
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
 325 330 335
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
 340 345 350
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
 355 360 365
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe
 370 375 380
 Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile
 385 390 395 400
 Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala
 405 410 415
 Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile
 420 425 430
 Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr
 435 440 445
 Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu
 450 455 460
 Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr
 465 470 475 480
 Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu
 485 490 495
 His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp
 500 505 510
 Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg
 515 520 525
 Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His
 530 535 540

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<222> (101)..(1057)
<223> RXA02319
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Met Ser Asn Tyr Ser 5															
acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163															
Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe 20															
gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211															
Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg 35															
gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259															
Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn 50															
gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac 307															
Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His 65															
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc 355															
Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly 85															
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa 403															
Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln 100															
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc 451															
Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg 115															
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa 499															
Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys 130															
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc 547															
Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg 145															
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc 595															
Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly 165															
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc 643															
Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg 180															

caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac 691
 Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp
 185 190 195

 gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac 739
 Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn
 200 205 210

 gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg 787
 Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met
 215 220 225

 caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa 835
 Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu
 230 235 240 245

 aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc 883
 Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr
 250 255 260

 ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc 931
 Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu
 265 270 275

 atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg 979
 Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met
 280 285 290

 acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa 1027
 Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu
 295 300 305

 ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atggggtcct 1077
 Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
 310 315

 aaa 1080

<210> 876

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 876

Met Ser Asn Tyr Ser Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala
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Thr Val Pro Gly Phe Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His
 20 25 30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
 35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
 50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
 65 70 75 80

Leu	Thr	Gly	Asn	Gly	Pro	Ser	Glu	Lys	Asp	Gly	Gly	Trp	Ala	Phe	Cys	
				85					90					95		
Ser	Gly	Gly	Asp	Gln	Arg	Ile	Arg	Gly	Arg	Ser	Gly	Tyr	Gln	Tyr	Ala	
				100					105					110		
Thr	Glu	His	Ala	Arg	Asp	Asp	Ala	Thr	Ala	Asp	Val	Phe	Thr	Val	Asp	
				115					120					125		
Ile	Ala	Arg	Thr	Lys	Val	Glu	Gly	Gly	Arg	Leu	His	Ile	Leu	Glu	Val	
				130					135					140		
Gln	Arg	Leu	Ile	Arg	Thr	Met	Pro	Lys	Val	Val	Ile	Ala	Val	Val	Asn	
				145					150					155		
Gly	Trp	Ala	Ala	Gly	Gly	Gly	His	Ser	Leu	His	Val	Val	Cys	Asp	Leu	
				165					170					175		
Thr	Ile	Ala	Ser	Arg	Gln	Glu	Ala	Arg	Phe	Lys	Gln	Thr	Asp	Ala	Asp	
				180					185					190		
Val	Gly	Ser	Phe	Asp	Ala	Gly	Tyr	Gly	Ser	Ala	Tyr	Leu	Ala	Lys	Met	
				195					200					205		
Val	Gly	Gln	Lys	Asn	Ala	Arg	Glu	Ile	Phe	Phe	Leu	Gly	Arg	Thr	Tyr	
				210					215					220		
Asp	Ala	Glu	Arg	Met	Gln	Gln	Met	Gly	Ala	Val	Asn	Ile	Val	Ala	Asp	
				225					230					235		
His	Gly	Asp	Leu	Glu	Lys	Glu	Ala	Ile	Gln	Ala	Ala	Arg	Glu	Ile	Asn	
				245					250					255		
Thr	Lys	Ser	Pro	Thr	Gly	Gln	Arg	Met	Leu	Lys	Phe	Ala	Phe	Asn	Leu	
				260					265					270		
Thr	Asp	Asp	Gly	Leu	Met	Gly	Gln	Gln	Val	Phe	Ala	Gly	Glu	Ala	Thr	
				275					280					285		
Arg	Leu	Ala	Tyr	Met	Thr	Asp	Glu	Ala	Val	Glu	Gly	Lys	Glu	Ala	Phe	
				290					295					300		
Leu	Glu	Lys	Arg	Glu	Pro	Asn	Trp	Asn	Glu	Phe	Pro	Tyr	Tyr	Tyr		
				305					310					315		

<210> 877

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) . . (994)

<223> RXS00393

<400> 877

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aattgcgcga tcgagtatgt gatggggaaa gatagagggtt atg tct cac acg gaa 115
Met Ser His Thr Glu

											1					5	
ccc	cag	ccg	aat	tct	gta	act	ttg	tcc	gat	tgg	att	caa	ggc	gca	cgc		163
Pro	Gln	Pro	Asn	Ser	Val	Thr	Leu	Ser	Asp	Trp	Ile	Gln	Gly	Ala	Arg		
			10						15					20			
ccg	cgt	acc	tgg	gca	aat	gcg	ttc	gcg	cct	gtc	att	gcc	ggg	tca	ggg		211
Pro	Arg	Thr	Trp	Ala	Asn	Ala	Phe	Ala	Pro	Val	Ile	Ala	Gly	Ser	Gly		
			25					30					35				
gtc	gcc	gct	ttt	cat	gat	ggg	ttt	gtg	tgg	tgg	aag	gcc	ttg	ctg	gcg		259
Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp	Lys	Ala	Leu	Leu	Ala		
		40					45					50					
ctt	gtc	gtg	gcg	tgg	gct	ttg	atc	atc	ggg	gtg	aat	tac	gcc	aat	gat		307
Leu	Val	Val	Ala	Trp	Ala	Leu	Ile	Ile	Gly	Val	Asn	Tyr	Ala	Asn	Asp		
	55					60					65						
tac	tct	gat	ggc	att	cgt	ggc	acc	gat	gaa	gac	cgc	acc	ggg	cct	ctg		355
Tyr	Ser	Asp	Gly	Ile	Arg	Gly	Thr	Asp	Glu	Asp	Arg	Thr	Gly	Pro	Leu		
	70				75					80					85		
cga	ctc	act	ggg	tct	ggg	ttg	gct	gag	ccg	aag	aaa	gtg	aaa	gct	gcg		403
Arg	Leu	Thr	Gly	Ser	Gly	Leu	Ala	Glu	Pro	Lys	Lys	Val	Lys	Ala	Ala		
				90					95					100			
gcg	ttt	att	tct	ttc	ggg	atc	gca	ggg	gtc	gcc	ggc	acc	gcg	ctg	agc		451
Ala	Phe	Ile	Ser	Phe	Gly	Ile	Ala	Gly	Val	Ala	Gly	Thr	Ala	Leu	Ser		
			105					110					115				
ctg	ttg	agc	gcg	tgg	tgg	ctg	atc	ctc	atc	ggc	atc	ctg	tgt	gtg	ctg		499
Leu	Leu	Ser	Ala	Trp	Trp	Leu	Ile	Leu	Ile	Gly	Ile	Leu	Cys	Val	Leu		
		120				125						130					
ggc	gcg	tgg	ttc	tac	acc	ggc	ggg	aaa	aat	cct	tat	ggg	tac	cgc	ggg		547
Gly	Ala	Trp	Phe	Tyr	Thr	Gly	Gly	Lys	Asn	Pro	Tyr	Gly	Tyr	Arg	Gly		
	135					140					145						
ctc	ggc	gag	att	gct	gtg	ttc	atc	ttc	ttc	ggc	ctc	gtc	gcg	gtc	atg		595
Leu	Gly	Glu	Ile	Ala	Val	Phe	Ile	Phe	Phe	Gly	Leu	Val	Ala	Val	Met		
	150				155					160					165		
gga	acg	cag	ttc	acc	caa	acc	ggg	tcc	gtc	agc	tgg	gcc	ggg	ttg	gcc		643
Gly	Thr	Gln	Phe	Thr	Gln	Thr	Gly	Ser	Val	Ser	Trp	Ala	Gly	Leu	Ala		
			170						175					180			
gcc	gca	gtt	ggc	gtg	ggg	tcg	atg	tct	gct	ggc	gtg	aac	ttg	gcc	aac		691
Ala	Ala	Val	Gly	Val	Gly	Ser	Met	Ser	Ala	Gly	Val	Asn	Leu	Ala	Asn		
			185					190					195				
aat	att	cgc	gat	att	cca	acc	gat	agc	aag	acc	gga	aaa	att	acc	ctc		739
Asn	Ile	Arg	Asp	Ile	Pro	Thr	Asp	Ser	Lys	Thr	Gly	Lys	Ile	Thr	Leu		
		200					205					210					
gcg	gtc	cgc	ctg	ggc	gat	gcg	ggg	gct	cgt	aag	ctg	ttc	ctc	gcg	ctg		787
Ala	Val	Arg	Leu	Gly	Asp	Ala	Gly	Ala	Arg	Lys	Leu	Phe	Leu	Ala	Leu		
	215					220					225						
att	tcc	acg	ccg	ttc	atc	atg	tcc	atc	tgc	ctg	gcg	ttt	gtc	gcc	tgg		835
Ile	Ser	Thr	Pro	Phe	Ile	Met	Ser	Ile	Cys	Leu	Ala	Phe	Val	Ala	Trp		
	230				235					240					245		

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cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
      250      255      260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc 931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile
      265      270      275

ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg 979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu
      280      285      290

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc 1017
Ala Leu Ala Phe Ser
      295

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<210> 878

<211> 298

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 878

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Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
  1          5          10          15

Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
      20      25      30

Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
      35      40      45

Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
      50      55      60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
      65      70      75      80

Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
      85      90      95

Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
      100      105      110

Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
      115      120      125

Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
      130      135      140

Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
      145      150      155      160

Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
      165      170      175

Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
      180      185      190

Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr

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195					200					205						
Gly	Lys	Ile	Thr	Leu	Ala	Val	Arg	Leu	Gly	Asp	Ala	Gly	Ala	Arg	Lys	
210					215					220						
Leu	Phe	Leu	Ala	Leu	Ile	Ser	Thr	Pro	Phe	Ile	Met	Ser	Ile	Cys	Leu	
225					230					235					240	
Ala	Phe	Val	Ala	Trp	Pro	Ala	Leu	Ile	Ala	Ile	Ile	Val	Phe	Pro	Leu	
245					250					255						
Ala	Leu	Lys	Ala	Ala	Gly	Pro	Ile	Arg	Asn	Asn	Ala	Thr	Gly	Lys	Asp	
260					265					270						
Leu	Ile	Pro	Val	Ile	Gly	Ser	Thr	Gly	Arg	Ala	Met	Ala	Leu	Trp	Ala	
275					280					285						
Val	Leu	Thr	Gly	Leu	Ala	Leu	Ala	Phe	Ser							
290					295											

<210> 879
 <211> 1005
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(982)
 <223> FRXA00393

<400> 879
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 aattgcgcgga tcgagtatgt gatggggaaa gatagagggtt atg tct cac acg gaa 115
 Met Ser His Thr Glu
 1 5
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50
 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
 55 60 65
 tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
 70 75 80 85
 cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
 90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
 105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
 120 125 130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
 135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
 150 155 160 165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
 170 175 180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
 185 190 195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
 200 205 210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
 215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
 230 235 240 245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
 250 255 260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
 265 270 275

gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
 Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp
 280 285 290

cat tagcggttag ctaaaacgct ttt 1005
 His

<210> 880

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 880

Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp

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Ile Gln Gly	Ala Arg Pro Arg Thr Trp	Ala Asn Ala Phe	Ala Pro Val
	20	25	30
Ile Ala Gly	Ser Gly Val Ala Ala Phe His Asp Gly	Phe Val Trp Trp	
	35	40	45
Lys Ala Leu	Leu Ala Leu Val Val Ala Trp Ala Leu	Ile Ile Gly Val	
	50	55	60
Asn Tyr Ala	Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp		
	65	70	75
Arg Thr Gly	Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys		
	85	90	95
Lys Val Lys	Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala		
	100	105	110
Gly Thr Ala	Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly		
	115	120	125
Ile Leu Cys	Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro		
	130	135	140
Tyr Gly Tyr	Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly		
	145	150	155
Leu Val Ala	Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser		
	165	170	175
Trp Ala Gly	Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly		
	180	185	190
Val Asn Leu	Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr		
	195	200	205
Gly Lys Ile	Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys		
	210	215	220
Leu Phe Leu	Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu		
	225	230	235
Ala Phe Val	Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu		
	245	250	255
Ala Leu Lys	Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp		
	260	265	270
Leu Ile Pro	Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro		
	275	280	285
Cys Ser Arg	Ala Trp His		
	290		

<210> 881

<211> 843

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(820)

<223> RXA00391

<400> 881

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tttcctcccc atccctgtac aagataaaaac ccgtgcacag ttg ctg cgc gat tct 115
                Leu Leu Arg Asp Ser
                1                    5

caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc 163
Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala
                10                    15                    20

act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg 211
Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu
                25                    30                    35

aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa 259
Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu
                40                    45                    50

ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag 307
Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln
                55                    60                    65

gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat 355
Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp
                70                    75                    80                    85

ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403
Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Glu
                90                    95                    100

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
                105                    110                    115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
                120                    125                    130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg
                135                    140                    145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
                150                    155                    160                    165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643
Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
                170                    175                    180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
                185                    190                    195

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att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
 200 205 210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
 215 220 225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
 230 235 240

tgc 843

<210> 882

<211> 240

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 882

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile
 1 5 10 15

Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala
 20 25 30

Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln
 35 40 45

Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His
 50 55 60

Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu
 65 70 75 80

Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala
 85 90 95

Gly Ala Ala Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser
 100 105 110

Leu Thr Pro Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile
 115 120 125

Glu Ala Leu Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu
 130 135 140

Ser Lys Gln Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val
 145 150 155 160

Thr Thr Tyr Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly
 165 170 175

Lys Pro Ile Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu
 180 185 190

Leu Gly Gly Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His
 195 200 205

Pro Asp Phe Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu

210	215	220
Leu His Asp Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Arg His		
225	230	235 240

<210> 883
 <211> 384
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(361)
 <223> RXS02908

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 gtgactggtc gcgtggatac ccgtcattga ttccggtgga ttg aag ttg cac cca 115
 Leu Lys Leu His Pro
 1 5
 gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163
 Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala
 10 15 20
 tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc 211
 Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala
 25 30 35
 gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac 259
 Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp
 40 45 50
 gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct 307
 Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser
 55 60 65
 ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355
 Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys
 70 75 80 85
 ctg ttt tagtcttcat tcttgctggc tgc 384
 Leu Phe

<210> 884
 <211> 87
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 884
 Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys
 1 5 10 15
 Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly

	20		25		30										
Gln	Ala	Ile	Val	Ala	Ala	Tyr	Ser	Gly	Ser	Ile	Ser	Pro	Ser	Glu	Val
	35						40					45			
Ile	Glu	Gly	Leu	Asp	Asp	Leu	Pro	Arg	Trp	Gln	Leu	Pro	Lys	Arg	Leu
	50					55					60				
Lys	His	Leu	Glu	Ser	Leu	Pro	Ser	Ile	Gly	Pro	Gly	Lys	Ala	Asp	Arg
	65				70					75					80
Arg	Ala	Ile	Ala	Lys	Leu	Phe									
				85											

<210> 885

<211> 705

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(682)

<223> RXA00997

<400> 885

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gcaccatgggt gctgaacaag tagccctata ctcggggcacc atg act aca tgg aaa 115
                                     Met Thr Thr Trp Lys
                                     1 5

gag ctc aca gat aac aac cca gcg cac tca gaa aac tac gcg cag cgc 163
Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu Asn Tyr Ala Gln Arg
                                     10 15 20

tgg cga aac ctc gcc gca gca ggc aat gat att tac ggc gaa gcc cgc 211
Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile Tyr Gly Glu Ala Arg
                                     25 30 35

ctc att gat gcc atg gca ccc agg gga gcg aaa atc ttg gat gct ggc 259
Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys Ile Leu Asp Ala Gly
                                     40 45 50

tgc ggc cag gga cgc atc ggt ggc tac ctg tcc aag caa ggc cac gat 307
Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser Lys Gln Gly His Asp
                                     55 60 65

gtt cta ggc aca gac ctt gat ccc atc ctg att gat tac gcc aag cag 355
Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile Asp Tyr Ala Lys Gln
                                     70 75 80 85

gac ttt cca gaa gct cgc tgg gtg gtg gga gat ctc tct gtt gat cag 403
Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp Leu Ser Val Asp Gln
                                     90 95 100

atc tca gag act gat ttt gat ctc att gtc tcc gcc ggc aac gtc atg 451
Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser Ala Gly Asn Val Met
                                     105 110 115

ggc ttt ctc gct gag gat ggt cgc gaa cct gca cta gcc aac att cac 499

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Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala Leu Ala Asn Ile His
 120 125 130

cgc gca ctg ggc gcc gat ggc cgc gct gtc atc ggt ttc ggc gca gga 547
 Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile Gly Phe Gly Ala Gly
 135 140 145

cgt gga tgg gtc ttt gga gac ttc ctc gaa gtc gca gaa cgc gtg ggc 595
 Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val Ala Glu Arg Val Gly
 150 155 160 165

ctc gag ttg gaa aat gct ttt gag tct tgg gat ctt aag cct ttt gtc 643
 Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp Leu Lys Pro Phe Val
 170 175 180

caa ggc tct gag ttc tta gtg gcg gta ttt acc aag aag taacacacct 692
 Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr Lys Lys
 185 190

atcttgcacc tga 705

<210> 886

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 886

Met Thr Thr Trp Lys Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu
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Asn Tyr Ala Gln Arg Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile
 20 25 30

Tyr Gly Glu Ala Arg Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys
 35 40 45

Ile Leu Asp Ala Gly Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser
 50 55 60

Lys Gln Gly His Asp Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile
 65 70 75 80

Asp Tyr Ala Lys Gln Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp
 85 90 95

Leu Ser Val Asp Gln Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser
 100 105 110

Ala Gly Asn Val Met Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala
 115 120 125

Leu Ala Asn Ile His Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile
 130 135 140

Gly Phe Gly Ala Gly Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val
 145 150 155 160

Ala Glu Arg Val Gly Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp
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Leu Lys Pro Phe Val Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr
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Lys Lys

<210> 887

<211> 861

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(838)

<223> RXA02189

<400> 887

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 Val Asp Ala Ala Asp
 1 5
 tat cac gaa cgc cac cct tct tat tta ggc acg gat tcc gct cac ggc 163
 Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr Asp Ser Ala His Gly
 10 15 20
 gag ttc tac tgg tgc ccc gag atg ctg cat gaa aaa gat gta cgt ctt 211
 Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu Lys Asp Val Arg Leu
 25 30 35
 ctt ggc act ccc gca gca ctc tcc ggc aag aaa att tta gag atc ggt 259
 Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys Ile Leu Glu Ile Gly
 40 45 50
 tgc ggc tgc gca ccg tgt gct cgg tgg ctg gcc aat gat gtt ccg aat 307
 Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala Asn Asp Val Pro Asn
 55 60 65
 gcc ttt gtc acc gct ttc gac att tct tca caa atg ctc aaa tac gca 355
 Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln Met Leu Lys Tyr Ala
 70 75 80 85
 ggt cac gac cat aac gta cac ctc gta cag gcc gat gca atg tca ctc 403
 Gly His Asp His Asn Val His Leu Val Gln Ala Asp Ala Met Ser Leu
 90 95 100
 ccc tac gcc gac agt tcc ttt gac gtg gtc ttt tcc gtt ttc ggc gcc 451
 Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe Ser Val Phe Gly Ala
 105 110 115
 atc ccc ttt gtg gag gat tcc gcc gca ctc atg aag gaa atc gcg cgc 499
 Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met Lys Glu Ile Ala Arg
 120 125 130
 gtc ctc aaa ccc ggc gga cgc ctc att ttc tcc atc acc cac ccg atg 547
 Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser Ile Thr His Pro Met
 135 140 145
 cgc tgg att ttc ctc gac gat ccc ggc ccc gca ggc ctc acc gcg atc 595

Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala Gly Leu Thr Ala Ile
 150 155 160 165
 acc agc tac ttc gac cag cgc ggc tac gtc gaa gaa gac gag gaa acc 643
 Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu Glu Asp Glu Glu Thr
 170 175 180
 ggt gct tta agc tat gcg gaa cag cac cgc acc atg ggc gcg cgg atc 691
 Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr Met Gly Ala Arg Ile
 185 190 195
 aat gag ctt atc gac gcc tcc ctc cac tta gat cac ctc atc gaa cca 739
 Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp His Leu Ile Glu Pro
 200 205 210
 gaa tgg cca gat gag ttg gaa gaa aac tgg ggc caa tgg tca cca ctt 787
 Glu Trp Pro Asp Glu Leu Glu Asn Trp Gly Gln Trp Ser Pro Leu
 215 220 225
 cga gga aag ctc ttc ccc ggg aca gca atc ttc ctc gcc acg tac cgc 835
 Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe Leu Ala Thr Tyr Arg
 230 235 240 245
 ccc taaaaaacca acggcgctca ttt 861
 Pro
 <210> 888
 <211> 246
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 888
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 Lys Asp Val Arg Leu Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys
 35 40 45
 Ile Leu Glu Ile Gly Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala
 50 55 60
 Asn Asp Val Pro Asn Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln
 65 70 75 80
 Met Leu Lys Tyr Ala Gly His Asp His Asn Val His Leu Val Gln Ala
 85 90 95
 Asp Ala Met Ser Leu Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe
 100 105 110
 Ser Val Phe Gly Ala Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met
 115 120 125
 Lys Glu Ile Ala Arg Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser
 130 135 140

Ile Thr His Pro Met Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala
 145 150 155 160

Gly Leu Thr Ala Ile Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu
 165 170 175

Glu Asp Glu Glu Thr Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr
 180 185 190

Met Gly Ala Arg Ile Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp
 195 200 205

His Leu Ile Glu Pro Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly
 210 215 220

Gln Trp Ser Pro Leu Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe
 225 230 235 240

Leu Ala Thr Tyr Arg Pro
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<210> 889
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(790)
 <223> RXA02311

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 Val Ala Lys Ala Asp
 1 5

tta gac aag gac ccc ttc gac gta gcg tca atg ttc gat gac gtc gga 163
 Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met Phe Asp Asp Val Gly
 10 15 20

aag aac tac gat ctc acc aat acc gtg ctt tct ttt ggt cag gac cgt 211
 Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser Phe Gly Gln Asp Arg
 25 30 35

gtg tgg cga aag cgc act agg cag cgc ctg gac ctc aag cca ggg gag 259
 Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp Leu Lys Pro Gly Glu
 40 45 50

aag gtg ctt gat cta gct gca gga aca gcc gtt tcc acc gtg gag ttg 307
 Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val Ser Thr Val Glu Leu
 55 60 65

gca aaa tcc ggc gcg ttt tgt gtg gcg tgt gat ttc tcc cag ggc atg 355
 Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp Phe Ser Gln Gly Met
 70 75 80 85

ctc gcc gca ggt aaa gac cgc gat gtg tcc aag gtt gtg ggc gat ggc 403
 Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys Val Val Gly Asp Gly

90										95					100					
atg	cag	ttg	cgc	ttt	gca	gac	aac	agc	ttt	gat	gct	gtg	acc	att	tct	451				
Met	Gln	Leu	Pro	Phe	Ala	Asp	Asn	Ser	Phe	Asp	Ala	Val	Thr	Ile	Ser					
			105				110						115							
tat	ggg	ctg	cgc	aat	att	cac	gat	ttc	cgc	gct	ggc	ctg	aaa	gaa	atg	499				
Tyr	Gly	Leu	Arg	Asn	Ile	His	Asp	Phe	Arg	Ala	Gly	Leu	Lys	Glu	Met					
			120				125						130							
gcc	cgc	gtg	act	aaa	cct	ggg	gga	cgc	ctc	acc	gtg	gcg	gag	ttc	tcc	547				
Ala	Arg	Val	Thr	Lys	Pro	Gly	Gly	Arg	Leu	Thr	Val	Ala	Glu	Phe	Ser					
			135				140						145							
acc	ccc	gtg	atc	cct	gtg	ttc	ggc	acc	gtg	tac	aag	gag	tac	ctc	atg	595				
Thr	Pro	Val	Ile	Pro	Val	Phe	Gly	Thr	Val	Tyr	Lys	Glu	Tyr	Leu	Met					
150				155						160			165							
cgc	ctg	ctg	ccc	cag	gcg	gcg	cgc	gca	gta	tcg	tcc	aac	ccg	gag	gcc	643				
Arg	Leu	Leu	Pro	Gln	Ala	Ala	Arg	Ala	Val	Ser	Ser	Asn	Pro	Glu	Ala					
			170				175						180							
tac	att	tac	ctg	gct	gat	tcc	atc	cgc	gca	tgg	cct	agc	cag	gcg	gaa	691				
Tyr	Ile	Tyr	Leu	Ala	Asp	Ser	Ile	Arg	Ala	Trp	Pro	Ser	Gln	Ala	Glu					
			185				190						195							
cta	gca	cgg	gag	atc	aac	cag	aat	ggg	tgg	tca	gat	tgc	ggg	tgg	cag	739				
Leu	Ala	Arg	Glu	Ile	Asn	Gln	Asn	Gly	Trp	Ser	Asp	Cys	Gly	Trp	Gln					
			200				205						210							
aac	ctg	acc	ttc	ggc	atc	gtc	gcg	ctg	cac	tcg	gcg	att	aaa	cca	gag	787				
Asn	Leu	Thr	Phe	Gly	Ile	Val	Ala	Leu	His	Ser	Ala	Ile	Lys	Pro	Glu					
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aac	tagtcgagtc	ccacagaggg	gag												813					
Asn																				
230																				

<210> 890

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 890

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Phe	Asp	Asp	Val	Gly	Lys	Asn	Tyr	Asp	Leu	Thr	Asn	Thr	Val	Leu	Ser
			20					25					30		

Phe	Gly	Gln	Asp	Arg	Val	Trp	Arg	Lys	Arg	Thr	Arg	Gln	Arg	Leu	Asp
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Leu	Lys	Pro	Gly	Glu	Lys	Val	Leu	Asp	Leu	Ala	Ala	Gly	Thr	Ala	Val
	50					55					60				

Ser	Thr	Val	Glu	Leu	Ala	Lys	Ser	Gly	Ala	Phe	Cys	Val	Ala	Cys	Asp
65					70				75					80	

Phe	Ser	Gln	Gly	Met	Leu	Ala	Ala	Gly	Lys	Asp	Arg	Asp	Val	Ser	Lys
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85								90				95			
Val	Val	Gly	Asp	Gly	Met	Gln	Leu	Pro	Phe	Ala	Asp	Asn	Ser	Phe	Asp
			100					105					110		
Ala	Val	Thr	Ile	Ser	Tyr	Gly	Leu	Arg	Asn	Ile	His	Asp	Phe	Arg	Ala
		115					120					125			
Gly	Leu	Lys	Glu	Met	Ala	Arg	Val	Thr	Lys	Pro	Gly	Gly	Arg	Leu	Thr
	130					135					140				
Val	Ala	Glu	Phe	Ser	Thr	Pro	Val	Ile	Pro	Val	Phe	Gly	Thr	Val	Tyr
145					150				155						160
Lys	Glu	Tyr	Leu	Met	Arg	Leu	Leu	Pro	Gln	Ala	Ala	Arg	Ala	Val	Ser
				165				170						175	
Ser	Asn	Pro	Glu	Ala	Tyr	Ile	Tyr	Leu	Ala	Asp	Ser	Ile	Arg	Ala	Trp
			180					185					190		
Pro	Ser	Gln	Ala	Glu	Leu	Ala	Arg	Glu	Ile	Asn	Gln	Asn	Gly	Trp	Ser
		195					200					205			
Asp	Cys	Gly	Trp	Gln	Asn	Leu	Thr	Phe	Gly	Ile	Val	Ala	Leu	His	Ser
	210					215					220				
Ala	Ile	Lys	Pro	Glu	Asn										
225					230										

<210> 891

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXN02912

<400> 891

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				Val	Thr	Ser	Pro	Glu	
				1				5	

tta	caa	aac	atc	ctt	aac	aat	tat	tgg	agc	ggc	agg	gca	gag	gct	tac	163
Leu	Gln	Asn	Ile	Leu	Asn	Asn	Tyr	Trp	Ser	Gly	Arg	Ala	Glu	Ala	Tyr	
			10					15					20			

cac	ctc	aac	caa	acc	caa	agc	gag	cgt	gca	caa	ttt	gaa	cgc	ccc	atc	211
His	Leu	Asn	Gln	Thr	Gln	Ser	Glu	Arg	Ala	Gln	Phe	Glu	Arg	Pro	Ile	
			25				30					35				

tgg	gaa	aag	gtg	tgg	tcg	aag	gct	ttg	cct	atc	gtg	tcg	gaa	gaa	gcg	259
Trp	Glu	Lys	Val	Trp	Ser	Lys	Ala	Leu	Pro	Ile	Val	Ser	Glu	Glu	Ala	
		40					45					50				

gta	aag	gtt	ctc	gat	ctt	ggc	tgt	ggc	gct	ggt	tat	gtc	acc	cac	ctt	307
Val	Lys	Val	Leu	Asp	Leu	Gly	Cys	Gly	Ala	Gly	Tyr	Val	Thr	His	Leu	

55	60	65	
cta agc gat tgc gga tac gaa aca atc ggc gtt gat ggt tct gag gaa			355
Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val Asp Gly Ser Glu Glu			
70	75	80	85
atg atc aat caa gct acg cag gag aat ggt ctt cgc agg tcg acg ggt			403
Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu Arg Arg Ser Thr Gly			
	90	95	100
cgg gcg act gcc att ttt cag gtc ggg gat gcg cat gat ccc gag ttc			451
Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala His Asp Pro Glu Phe			
	105	110	115
cgg gaa ggc tct ttt gat gcg ata acc agc cgg tat gtg ttg tgg act			499
Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg Tyr Val Leu Trp Thr			
	120	125	130
ctg ctg gat ccc cag gca gcg att aat cgt tgg gtg tct ttg cta aaa			547
Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp Val Ser Leu Leu Lys			
	135	140	145
cct ggt ggg gtt att gcg tgc gta gat gcg gct tgg tat ccg aag ggc			595
Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala Trp Tyr Pro Lys Gly			
	150	155	160
att gat gct ggc acg gaa gta gat tca gtg gat ggt ccg agt gct ttc			643
Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp Gly Pro Ser Ala Phe			
	170	175	180
gta gag acc tat acc ccg gaa ctt ttg agg aat ctt ccc atg tca acg			691
Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn Leu Pro Met Ser Thr			
	185	190	195
acc tcc act ggc cac aat ttc gca gag ctt ttc cac aac gct ggc ctc			739
Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe His Asn Ala Gly Leu			
	200	205	210
aaa gaa gtc aca ttg aca ccc att gag ggg ctg gct gaa ctt gac cag			787
Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu Ala Glu Leu Asp Gln			
	215	220	225
cga ttt ggc ctc tca cca ggg cat gag tcg act ccg cag ttc cta ttc			835
Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr Pro Gln Phe Leu Phe			
	230	235	240
agg gga att aaa tcc agt tagtgctggt ttaagcggtc gag			876
Arg Gly Ile Lys Ser Ser			
	250		

<210> 892

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 892

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20					25					30						
Phe	Glu	Arg	Pro	Ile	Trp	Glu	Lys	Val	Trp	Ser	Lys	Ala	Leu	Pro	Ile	
35					40					45						
Val	Ser	Glu	Glu	Ala	Val	Lys	Val	Leu	Asp	Leu	Gly	Cys	Gly	Ala	Gly	
50					55					60						
Tyr	Val	Thr	His	Leu	Leu	Ser	Asp	Cys	Gly	Tyr	Glu	Thr	Ile	Gly	Val	
65					70					75					80	
Asp	Gly	Ser	Glu	Glu	Met	Ile	Asn	Gln	Ala	Thr	Gln	Glu	Asn	Gly	Leu	
85					90					95						
Arg	Arg	Ser	Thr	Gly	Arg	Ala	Thr	Ala	Ile	Phe	Gln	Val	Gly	Asp	Ala	
100					105					110						
His	Asp	Pro	Glu	Phe	Arg	Glu	Gly	Ser	Phe	Asp	Ala	Ile	Thr	Ser	Arg	
115					120					125						
Tyr	Val	Leu	Trp	Thr	Leu	Leu	Asp	Pro	Gln	Ala	Ala	Ile	Asn	Arg	Trp	
130					135					140						
Val	Ser	Leu	Leu	Lys	Pro	Gly	Gly	Val	Ile	Ala	Cys	Val	Asp	Ala	Ala	
145					150					155					160	
Trp	Tyr	Pro	Lys	Gly	Ile	Asp	Ala	Gly	Thr	Glu	Val	Asp	Ser	Val	Asp	
165					170					175						
Gly	Pro	Ser	Ala	Phe	Val	Glu	Thr	Tyr	Thr	Pro	Glu	Leu	Leu	Arg	Asn	
180					185					190						
Leu	Pro	Met	Ser	Thr	Thr	Ser	Thr	Gly	His	Asn	Phe	Ala	Glu	Leu	Phe	
195					200					205						
His	Asn	Ala	Gly	Leu	Lys	Glu	Val	Thr	Leu	Thr	Pro	Ile	Glu	Gly	Leu	
210					215					220						
Ala	Glu	Leu	Asp	Gln	Arg	Phe	Gly	Leu	Ser	Pro	Gly	His	Glu	Ser	Thr	
225					230					235					240	
Pro	Gln	Phe	Leu	Phe	Arg	Gly	Ile	Lys	Ser	Ser						
245					250											

<210> 893

<211> 585

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> RXS00998

<400> 893

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	Met Thr Ser Arg Asp	
	1 5	

gat caa ccc caa gat ctg ctt tcg ctt gca gaa ctt gcc gcc acc aga 163
Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu Leu Ala Ala Thr Arg
10 15 20
gct tta acc aca gac gaa ctt gaa gca ctc aac aac gcc aat tat ggc 211
Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly
25 30 35
ctc gac cgc aat ctg ggg ctg cgc tac acc acc atc gag ccc ggc cgg 259
Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg
40 45 50
gtg gtc agc gaa ctt cac gtg gca tcc aag cac ctg caa gtg gtg ggc 307
Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly
55 60 65
ttg gtc aac ggt ggt gtc tac gcc gcc atc gcc gaa tcc act gga tca 355
Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala Glu Ser Thr Gly Ser
70 75 80 85
gtc gcc agc atg att tcc gcc cct gga aaa atg gtc gtc ggc atc aac 403
Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met Val Val Gly Ile Asn
90 95 100
aac aac acc gac ttc att tct gct gtg agc tcc ggt gtc atc gtg gcc 451
Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser Gly Val Ile Val Ala
105 110 115
gaa gca acg ccg att cag cta ggt ggc cgc acc cat ctg tgg cag atc 499
Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr His Leu Trp Gln Ile
120 125 130
gaa tgc acc cac cgc gga gaa gtc gtc gca cga acc aca ctg cgc acc 547
Glu Cys Thr His Arg Gly Glu Val Val Ala Arg Thr Thr Leu Arg Thr
135 140 145
atg gtg ctg aac aag tagccctata ctcgggcacc atg 585
Met Val Leu Asn Lys
150

<210> 894

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 894

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20 25 30
Asn Ala Asn Tyr Gly Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr
35 40 45
Ile Glu Pro Gly Arg Val Val Ser Glu Leu His Val Ala Ser Lys His
50 55 60
Leu Gln Val Val Gly Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala

65		70		75		80
Glu Ser Thr Gly	Ser Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met					
	85			90		95
Val Val Gly Ile	Asn Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser					
	100		105		110	
Gly Val Ile Val	Ala Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr					
	115		120		125	
His Leu Trp Gln	Ile Glu Cys Thr His Arg Gly Glu Val Val Ala Arg					
	130		135		140	
Thr Thr Leu Arg	Thr Met Val Leu Asn Lys					
145		150				

<210> 895

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA01215

<400> 895

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cccaaaacgt ccacaaccag gaaggctaag caggatcctc atg act gct cac tgg 115
                                         Met Thr Ala His Trp
                                         1           5

aaa caa aac caa aag aac ctc atg ctg ttt tcg ggt cgt gcg cac cca 163
Lys Gln Asn Gln Lys Asn Leu Met Leu Phe Ser Gly Arg Ala His Pro
                        10                        15                        20

gaa ctg gca gaa gct gta gct aaa gag ctc gac gtc aac gtc acc cca 211
Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp Val Asn Val Thr Pro
                        25                        30                        35

atg acg gca cgc gat ttc gcc aac ggt gaa atc tac gtc cgc ttc gag 259
Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile Tyr Val Arg Phe Glu
                        40                        45                        50

gaa tca gtt cgt ggc tcc gac tgc ttc gtc ctg cag tcc cac acc cag 307
Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu Gln Ser His Thr Gln
                        55                        60                        65

cct ctc aac aag tgg ctc atg gaa cag ctg ctg atg atc gac gct ttg 355
Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu Met Ile Asp Ala Leu
                        70                        75                        80                        85

aag cgt ggt tcc gca aag cgc atc acc gcg atc ctg ccg ttc tac cca 403
Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile Leu Pro Phe Tyr Pro
                        90                        95                        100

tat gcc cgc cag gac aag aag cac cgc ggc cgc gag cca att tct gct 451
Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg Glu Pro Ile Ser Ala

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105						110						115						
cgc	ctc	atc	gcc	gac	ctc	atg	ctc	acc	gct	ggc	gcg	gac	cgt	atc	gtg	499		
Arg	Leu	Ile	Ala	Asp	Leu	Met	Leu	Thr	Ala	Gly	Ala	Asp	Arg	Ile	Val			
120						125						130						
tcc	gtg	gac	ttg	cac	acc	gat	cag	atc	cag	ggc	ttc	ttc	gac	ggc	cca	547		
Ser	Val	Asp	Leu	His	Thr	Asp	Gln	Ile	Gln	Gly	Phe	Phe	Asp	Gly	Pro			
135						140						145						
gtc	gat	cac	atg	cac	gcc	atg	ccg	atc	ctc	acc	gat	cac	atc	aag	gaa	595		
Val	Asp	His	Met	His	Ala	Met	Pro	Ile	Leu	Thr	Asp	His	Ile	Lys	Glu			
150						155						160						165
aac	tac	aac	ctg	gac	aac	atc	tgc	gtg	gtc	tcc	cct	gac	gca	ggt	cgc	643		
Asn	Tyr	Asn	Leu	Asp	Asn	Ile	Cys	Val	Val	Ser	Pro	Asp	Ala	Gly	Arg			
170						175						180						
gtg	aag	gtt	gca	gag	aag	tgg	gct	aac	acc	ttg	ggc	gat	gcc	cca	atg	691		
Val	Lys	Val	Ala	Glu	Lys	Trp	Ala	Asn	Thr	Leu	Gly	Asp	Ala	Pro	Met			
185						190						195						
gcg	ttc	gtg	cac	aag	acc	cgc	tcc	acc	gag	gta	gca	aac	cag	gtt	gtc	739		
Ala	Phe	Val	His	Lys	Thr	Arg	Ser	Thr	Glu	Val	Ala	Asn	Gln	Val	Val			
200						205						210						
gcc	aac	cgc	gtc	gtc	ggg	gac	gtc	gac	ggc	aag	gac	tgc	gtg	ctt	ctc	787		
Ala	Asn	Arg	Val	Val	Gly	Asp	Val	Asp	Gly	Lys	Asp	Cys	Val	Leu	Leu			
215						220						225						
gac	gac	atg	atc	gac	act	ggc	ggc	acc	atc	gcc	ggc	gct	gtg	ggc	gtc	835		
Asp	Asp	Met	Ile	Asp	Thr	Gly	Gly	Thr	Ile	Ala	Gly	Ala	Val	Gly	Val			
230						235						240						245
ctg	aag	aag	gct	ggc	gca	aag	tca	gtc	gtc	atc	gcc	tgc	acc	cac	ggt	883		
Leu	Lys	Lys	Ala	Gly	Ala	Lys	Ser	Val	Val	Ile	Ala	Cys	Thr	His	Gly			
250						255						260						
gtg	ttc	tct	gac	cca	gcc	cgc	gag	cgc	ctg	tct	gca	tgc	ggg	gct	gaa	931		
Val	Phe	Ser	Asp	Pro	Ala	Arg	Glu	Arg	Leu	Ser	Ala	Cys	Gly	Ala	Glu			
265						270						275						
gaa	gtc	atc	acc	acc	gac	acc	ctg	cca	cag	tcc	acc	gag	ggc	tgg	agc	979		
Glu	Val	Ile	Thr	Thr	Asp	Thr	Leu	Pro	Gln	Ser	Thr	Glu	Gly	Trp	Ser			
280						285						290						
aac	ctg	acc	gtt	ttg	tcg	atc	gca	ccg	ctg	ctg	gct	cgc	acc	atc	aac	1027		
Asn	Leu	Thr	Val	Leu	Ser	Ile	Ala	Pro	Leu	Leu	Ala	Arg	Thr	Ile	Asn			
295						300						305						
gag	atc	ttc	gaa	aac	ggg	tcc	gtc	acc	acc	ctc	ttc	gag	ggc	gag	gcc	1075		
Glu	Ile	Phe	Glu	Asn	Gly	Ser	Val	Thr	Thr	Leu	Phe	Glu	Gly	Glu	Ala			
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<210> 896

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 896

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Val	Asn	Val	Thr	Pro	Met	Thr	Ala	Arg	Asp	Phe	Ala	Asn	Gly	Glu	Ile
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Tyr	Val	Arg	Phe	Glu	Glu	Ser	Val	Arg	Gly	Ser	Asp	Cys	Phe	Val	Leu
	50					55					60				
Gln	Ser	His	Thr	Gln	Pro	Leu	Asn	Lys	Trp	Leu	Met	Glu	Gln	Leu	Leu
65					70					75					80
Met	Ile	Asp	Ala	Leu	Lys	Arg	Gly	Ser	Ala	Lys	Arg	Ile	Thr	Ala	Ile
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Leu	Pro	Phe	Tyr	Pro	Tyr	Ala	Arg	Gln	Asp	Lys	Lys	His	Arg	Gly	Arg
			100					105					110		
Glu	Pro	Ile	Ser	Ala	Arg	Leu	Ile	Ala	Asp	Leu	Met	Leu	Thr	Ala	Gly
		115					120					125			
Ala	Asp	Arg	Ile	Val	Ser	Val	Asp	Leu	His	Thr	Asp	Gln	Ile	Gln	Gly
	130					135					140				
Phe	Phe	Asp	Gly	Pro	Val	Asp	His	Met	His	Ala	Met	Pro	Ile	Leu	Thr
145					150					155					160
Asp	His	Ile	Lys	Glu	Asn	Tyr	Asn	Leu	Asp	Asn	Ile	Cys	Val	Val	Ser
				165				170						175	
Pro	Asp	Ala	Gly	Arg	Val	Lys	Val	Ala	Glu	Lys	Trp	Ala	Asn	Thr	Leu
			180					185					190		
Gly	Asp	Ala	Pro	Met	Ala	Phe	Val	His	Lys	Thr	Arg	Ser	Thr	Glu	Val
		195					200					205			
Ala	Asn	Gln	Val	Val	Ala	Asn	Arg	Val	Val	Gly	Asp	Val	Asp	Gly	Lys
	210					215					220				
Asp	Cys	Val	Leu	Leu	Asp	Asp	Met	Ile	Asp	Thr	Gly	Gly	Thr	Ile	Ala
225					230					235					240
Gly	Ala	Val	Gly	Val	Leu	Lys	Lys	Ala	Gly	Ala	Lys	Ser	Val	Val	Ile
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Ala	Cys	Thr	His	Gly	Val	Phe	Ser	Asp	Pro	Ala	Arg	Glu	Arg	Leu	Ser
			260					265					270		
Ala	Cys	Gly	Ala	Glu	Glu	Val	Ile	Thr	Thr	Asp	Thr	Leu	Pro	Gln	Ser
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Thr	Glu	Gly	Trp	Ser	Asn	Leu	Thr	Val	Leu	Ser	Ile	Ala	Pro	Leu	Leu
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																Val Val Lys Lys Pro	5
																1	
gcg ggc atc gca gta ggc gat ggc gaa cag atc ctg gtt ttc aaa gat																163	
Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile Leu Val Phe Lys Asp																	
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ttg ggc cta gtc tcc caa gtt ttc gac caa cca att ctg gaa tcc ctc																211	
Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro Ile Leu Glu Ser Leu																	
																25 30 35	
cgc gga aac atc gcc atc gga cac acc cga tac acc acc gcc ggc gga																259	
Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr Thr Thr Ala Gly Gly																	
																40 45 50	
aac acc tgg gaa aat gcc cag cct atg ttc cgc atg gca cca gat ggc																307	
Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg Met Ala Pro Asp Gly																	
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acc gat atc gcc ctt gga cac aac ggc aac ctg att aat tac atc gag																355	
Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu Ile Asn Tyr Ile Glu																	
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ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc gat ccc gcc aag aag																403	
Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val Asp Pro Ala Lys Lys																	
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cca tca gat acc gat gtg ctc act gga ctg ctc gca agc ggc gtc cat																451	
Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu Ala Ser Gly Val His																	
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Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu Leu Leu Pro Ser Val																	
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aag gga gcc tac tgc ctc acc ttc acc gac gga cac acc ctg tac gca																547	
Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly His Thr Leu Tyr Ala																	
																135 140 145	
gcg cgt gat cca ttc ggc atc cgc cca ctg tcc atc ggc cgc ctc gag																595	
Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser Ile Gly Arg Leu Glu																	
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Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala Leu Asp Ile Val Gly	
170 175 180	
gcc tcg cat gtg cgc gag gtc gaa cca ggc gaa ctg att gct atc gac	691
Ala Ser His Val Arg Glu Val Glu Pro Gly Glu Leu Ile Ala Ile Asp	
185 190 195	
gaa tcc ggc ctc aag tcc gca cga ttc gcc gag aca acc cgc aaa ggt	739
Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu Thr Thr Arg Lys Gly	
200 205 210	
tgc gtc ttc gaa tac gtt tac ctg gct cgt cca gac tcc gtg atc aag	787
Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro Asp Ser Val Ile Lys	
215 220 225	
gga aga aac gtc aac gaa gcc cga ctt gaa atc ggc cgc aag ctc gct	835
Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile Gly Arg Lys Leu Ala	
230 235 240 245	
gca gaa gca cca gca gtc ggc gat cta gtc atc cca acc cca gaa tca	883
Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile Pro Thr Pro Glu Ser	
250 255 260	
ggc acc cca gca gca gtt gga ttc gcc caa gca tct ggc atc cca ttc	931
Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala Ser Gly Ile Pro Phe	
265 270 275	
ggc caa ggc atg gtc aaa aac gcc tac gtt ggc cga acc ttc atc cag	979
Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly Arg Thr Phe Ile Gln	
280 285 290	
cct tcc gac act ctc cgc caa ctg gga atc cgc ctc aag ctg aac cca	1027
Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg Leu Lys Leu Asn Pro	
295 300 305	
ttg cgc gag gtt atc gcc gga aag cgc ctt gtg gtt gtg gat gat tcc	1075
Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val Val Val Asp Asp Ser	
310 315 320 325	
atc gtc cgc ggt aac acc caa cgc gcc gtg atc cgc atg ttg cgc gaa	1123
Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile Arg Met Leu Arg Glu	
330 335 340	
gcc ggt gca gct gag gtt cac gta cgc atc gcc tca cca ccc gtg aaa	1171
Ala Gly Ala Ala Glu Val His Val Arg Ile Ala Ser Pro Pro Val Lys	
345 350 355	
tgg cca tgc ttc tac ggc atc gat ttt gcc acc cca ggc gaa ctc att	1219
Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr Pro Gly Glu Leu Ile	
360 365 370	
gcc aac gct gtc acc agt gac aac gaa gca gaa atg gta gaa gca gtc	1267
Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu Met Val Glu Ala Val	
375 380 385	
cgc tcc gca atc ggc gca gac acc ctc ggc tac gtc tcc atc gac tcc	1315
Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr Val Ser Ile Asp Ser	
390 395 400 405	

atg gtt gca gca acc gag caa cca gcc aac gaa ctc tgc atc gcc tgc 1363
Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu Leu Cys Ile Ala Cys
410 415 420

ttc gac ggc aaa tac ccc atg ggt ctg cca cag gga aac agc aac gca 1411
Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln Gly Asn Ser Asn Ala
425 430 435

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<210> 898

<211> 449

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 898

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35 40 45

Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
50 55 60

Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
65 70 75 80

Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val
85 90 95

Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu
100 105 110

Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu
115 120 125

Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
130 135 140

His Thr Leu Tyr Ala Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser
145 150 155 160

Ile Gly Arg Leu Glu Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala
165 170 175

Leu Asp Ile Val Gly Ala Ser His Val Arg Glu Val Glu Pro Gly Glu
180 185 190

Leu Ile Ala Ile Asp Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu
195 200 205

Thr Thr Arg Lys Gly Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro

210					215					220						
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Gly	Arg	Lys	Leu	Ala	Ala	Glu	Ala	Pro	Ala	Val	Gly	Asp	Leu	Val	Ile	
				245					250				255			
Pro	Thr	Pro	Glu	Ser	Gly	Thr	Pro	Ala	Ala	Val	Gly	Phe	Ala	Gln	Ala	
			260					265					270			
Ser	Gly	Ile	Pro	Phe	Gly	Gln	Gly	Met	Val	Lys	Asn	Ala	Tyr	Val	Gly	
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Arg	Thr	Phe	Ile	Gln	Pro	Ser	Asp	Thr	Leu	Arg	Gln	Leu	Gly	Ile	Arg	
		290					295					300				
Leu	Lys	Leu	Asn	Pro	Leu	Arg	Glu	Val	Ile	Ala	Gly	Lys	Arg	Leu	Val	
305					310					315				320		
Val	Val	Asp	Asp	Ser	Ile	Val	Arg	Gly	Asn	Thr	Gln	Arg	Ala	Val	Ile	
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Arg	Met	Leu	Arg	Glu	Ala	Gly	Ala	Ala	Glu	Val	His	Val	Arg	Ile	Ala	
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Ser	Pro	Pro	Val	Lys	Trp	Pro	Cys	Phe	Tyr	Gly	Ile	Asp	Phe	Ala	Thr	
			355				360					365				
Pro	Gly	Glu	Leu	Ile	Ala	Asn	Ala	Val	Thr	Ser	Asp	Asn	Glu	Ala	Glu	
			370				375					380				
Met	Val	Glu	Ala	Val	Arg	Ser	Ala	Ile	Gly	Ala	Asp	Thr	Leu	Gly	Tyr	
385					390					395				400		
Val	Ser	Ile	Asp	Ser	Met	Val	Ala	Ala	Thr	Glu	Gln	Pro	Ala	Asn	Glu	
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Leu	Cys	Ile	Ala	Cys	Phe	Asp	Gly	Lys	Tyr	Pro	Met	Gly	Leu	Pro	Gln	
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Ser

<210> 899

<211> 524

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (61)..(501)

<223> FRXA00558

<400> 899

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Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile
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ctg gtt ttc aaa gat ttg ggc cta gtc tcc caa gtt ttc gac caa cca 156
Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro
          20          25          30

att ctg gaa tcc ctc cgc gga aac atc gcc atc gga cac acc cga tac 204
Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr
          35          40          45

acc acc gcc ggc gga aac acc tgg gaa aat gcc cag cct atg ttc cgc 252
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
          50          55          60

atg gca cca gat ggc acc gat atc gcc ctt gga cac aac ggc aac ctg 300
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
  65          70          75          80

att aat tac atc gag ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc 348
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val
          85          90          95

gat ccc gcc aag aag cca tca gat acc gat gtg ctc act gga ctg ctc 396
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu
          100          105          110

gca agc ggc gtc cat gac gga aat aat ctc ttt gat tcc gcc aag gaa 444
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu
          115          120          125

ctc ctc ccc agc gtc aag gga gcc tac tgc ctc acc ttc acc gac gga 492
Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
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<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 900

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Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro
          20          25          30

Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr
          35          40          45

Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
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Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
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				Met	Arg	Ile	Leu	Val								
				1				5								
atc	ggc	tcg	ggc	gcc	cgt	gag	cac	gcc	ctc	ctc	cgt	gga	ctg	tca	act	163
Ile	Gly	Ser	Gly	Ala	Arg	Glu	His	Ala	Leu	Leu	Arg	Gly	Leu	Ser	Thr	
				10					15					20		
gac	cct	gca	acc	act	gaa	ctc	cac	gtt	gcc	cca	ggt	aac	gct	ggt	ctt	211
Asp	Pro	Ala	Thr	Thr	Glu	Leu	His	Val	Ala	Pro	Gly	Asn	Ala	Gly	Leu	
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gga	tcg	atc	gca	act	gtc	cac	cct	ggc	atc	aag	gct	gat	gat	cca	gag	259
Gly	Ser	Ile	Ala	Thr	Val	His	Pro	Gly	Ile	Lys	Ala	Asp	Asp	Pro	Glu	
		40					45					50				
gct	gtc	act	gcg	ttg	gct	aaa	gaa	ctg	aac	tct	gat	ctg	ggt	ggt	atc	307
Ala	Val	Thr	Ala	Leu	Ala	Lys	Glu	Leu	Asn	Ser	Asp	Leu	Val	Val	Ile	
		55				60					65					
ggc	cca	gag	atc	cct	ttg	gtt	gcg	ggt	gtt	gct	gat	gca	ctt	cgc	gcg	355
Gly	Pro	Glu	Ile	Pro	Leu	Val	Ala	Gly	Val	Ala	Asp	Ala	Leu	Arg	Ala	
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gcg	ggt	atc	gct	gtg	ttt	ggt	cct	aac	aag	gac	gct	gct	cgt	atc	gag	403
Ala	Gly	Ile	Ala	Val	Phe	Gly	Pro	Asn	Lys	Asp	Ala	Ala	Arg	Ile	Glu	
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Gly	Ser	Lys	Ala	Phe	Ala	Lys	Asp	Val	Met	Ala	Ala	Gln	Gly	Val	Arg	
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Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp Val Val Lys Asp Asp	
135 140 145	
ggt ttg tct gcg ggc aag ggt gtt gtg gtt acc ccc gat cgt gca gca	595
Gly Leu Ser Ala Gly Lys Gly Val Val Val Thr Pro Asp Arg Ala Ala	
150 155 160 165	
gca cgt gct cac gta gat gca gtg ctt gag ggc gga aat cca gtt ttg	643
Ala Arg Ala His Val Asp Ala Val Leu Glu Gly Gly Asn Pro Val Leu	
170 175 180	
ctg gag tcc ttc ctt gat ggc cct gag gtt tcc ctg ttc tgc ctg gtt	691
Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu Phe Cys Leu Val	
185 190 195	
gat ggc gag acg gta gtt cct ctg ctg cca gcg cag gat cac aag cgt	739
Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln Asp His Lys Arg	
200 205 210	
gcg tac gac aac gat gag ggc cca aac act ggt ggc atg ggt gct tat	787
Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly Met Gly Ala Tyr	
215 220 225	
gcg ccg ctt cct tgg ctg cct gaa gat ggc gtc cag cgc att gtc gat	835
Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln Arg Ile Val Asp	
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Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala Arg Gly Cys Ala	
250 255 260	
tac tcc ggt ctg ctt tac gca ggt atc gca tgg ggt gca gaa ggc cct	931
Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly Ala Glu Gly Pro	
265 270 275	
gca gta gtg gag ttc aac tgc cgc ttc ggc gat cca gaa acc cag gct	979
Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro Glu Thr Gln Ala	
280 285 290	
gta ctg gca cta ctg aag act cct cta gca gta ctg ctc aac gca gtt	1027
Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu Leu Asn Ala Val	
295 300 305	
gct act gga acc ttg gca gag cag cca gca ctg gag tgg gag gat gct	1075
Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu Trp Glu Asp Ala	
310 315 320 325	
tac gcc ctg act gtg gtg ttg gct tct tac aac tac cca gag gca cct	1123
Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr Pro Glu Ala Pro	
330 335 340	
cgt act ggt gat gtc atc cgc aac gct gat gca gat aac gtt ctt cac	1171
Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp Asn Val Leu His	
345 350 355	

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Asp	Leu	Val	Val	Ile	Gly	Pro	Glu	Ile	Pro	Leu	Val	Ala	Gly	Val	Ala
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Asp	Ala	Leu	Arg	Ala	Ala	Gly	Ile	Ala	Val	Phe	Gly	Pro	Asn	Lys	Asp
			85						90					95	
Ala	Ala	Arg	Ile	Glu	Gly	Ser	Lys	Ala	Phe	Ala	Lys	Asp	Val	Met	Ala
			100					105					110		
Ala	Gln	Gly	Val	Arg	Thr	Ala	His	Ala	Glu	Thr	Ile	Thr	Pro	Gly	Ala
		115					120					125			
Ser	Ser	Glu	Asp	Ile	Asp	Ala	Ala	Ile	Asp	Arg	Phe	Gly	Pro	Thr	Trp
	130					135					140				
Val	Val	Lys	Asp	Asp	Gly	Leu	Ser	Ala	Gly	Lys	Gly	Val	Val	Val	Thr
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Pro	Asp	Arg	Ala	Ala	Ala	Arg	Ala	His	Val	Asp	Ala	Val	Leu	Glu	Gly
				165					170					175	
Gly	Asn	Pro	Val	Leu	Leu	Glu	Ser	Phe	Leu	Asp	Gly	Pro	Glu	Val	Ser
			180					185					190		

Leu Phe Cys Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala
 195 200 205
 Gln Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly
 210 215 220
 Gly Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val
 225 230 235 240
 Gln Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val
 245 250 255
 Ala Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp
 260 265 270
 Gly Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp
 275 280 285
 Pro Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val
 290 295 300
 Leu Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu
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 Glu Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn
 325 330 335
 Tyr Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala
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 Asp Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu
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 Val Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr
 370 375 380
 Leu Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu
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 Met Arg Ile Leu Val

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atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act			163
Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr	10	20	
gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt			211
Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu	25	35	
gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag			259
Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu	40	50	
gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc			307
Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile	55	65	
ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg			355
Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala	70	85	
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Ala Gly Ile			

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 35 40 45
 Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser
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 Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala
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 Asp Ala Leu Arg Ala Ala Gly Ile
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Asn	Pro	Val	Leu	Leu	Glu	Ser	Phe	Leu	Asp	Gly	Pro	Glu	Val	Ser	Leu	
		20						25					30			
ttc	ttc	ctg	gtt	gat	ggc	gag	acg	gta	gtt	cct	ctg	ctg	cca	gcg	cag	144
Phe	Phe	Leu	Val	Asp	Gly	Glu	Thr	Val	Val	Pro	Leu	Leu	Pro	Ala	Gln	
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Asp	His	Lys	Arg	Ala	Tyr	Asp	Asn	Asp	Glu	Gly	Pro	Asn	Thr	Gly	Gly	
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Met	Gly	Ala	Tyr	Ala	Pro	Leu	Pro	Trp	Leu	Pro	Glu	Asp	Gly	Val	Gln	
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cgc	att	gtc	gat	gag	gtc	tgc	gtt	cct	gtt	gct	cgt	gag	atg	gtg	gca	288
Arg	Ile	Val	Asp	Glu	Val	Cys	Val	Pro	Val	Ala	Arg	Glu	Met	Val	Ala	
				85					90					95		
cgt	ggt	tgc	gcg	tac	tcc	ggt	ctg	ctt	tac	gca	ggt	atc	gca	tgg	ggt	336
Arg	Gly	Cys	Ala	Tyr	Ser	Gly	Leu	Leu	Tyr	Ala	Gly	Ile	Ala	Trp	Gly	
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gca	gaa	ggc	cct	gca	gta	gtg	gag	ttc	aac	tgc	cgc	ttc	ggc	gat	cca	384
Ala	Glu	Gly	Pro	Ala	Val	Val	Glu	Phe	Asn	Cys	Arg	Phe	Gly	Asp	Pro	
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gaa	acc	cag	gct	gta	ctg	gca	cta	ctg	aag	act	cct	cta	gca	gta	ctg	432
Glu	Thr	Gln	Ala	Val	Leu	Ala	Leu	Leu	Lys	Thr	Pro	Leu	Ala	Val	Leu	
	130					135					140					
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Leu	Asn	Ala	Val	Ala	Thr	Gly	Thr	Leu	Ala	Glu	Gln	Pro	Ala	Leu	Glu	
	145				150					155					160	
tgg	gag	gat	gct	tac	gcc	ctg	act	gtg	gtg	ttg	gct	tct	tac	aac	tac	528
Trp	Glu	Asp	Ala	Tyr	Ala	Leu	Thr	Val	Val	Leu	Ala	Ser	Tyr	Asn	Tyr	
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cca	gag	gca	cct	cgt	act	ggt	gat	gtc	atc	cgc	aac	gct	gat	gca	gat	576
Pro	Glu	Ala	Pro	Arg	Thr	Gly	Asp	Val	Ile	Arg	Asn	Ala	Asp	Ala	Asp	
			180					185					190			
aac	gtt	ctt	cac	gct	ggt	acc	gca	ctc	aat	gct	gaa	ggc	gag	ctg	gtc	624
Asn	Val	Leu	His	Ala	Gly	Thr	Ala	Leu	Asn	Ala	Glu	Gly	Glu	Leu	Val	
		195					200					205				
tct	gcg	ggc	ggt	cgt	gtt	ctt	aac	gtg	atc	ggt	gtg	ggt	gag	acc	ctg	672
Ser	Ala	Gly	Gly	Arg	Val	Leu	Asn	Val	Ile	Gly	Val	Gly	Glu	Thr	Leu	
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gag	gct	gca	cgc	gat	aac	gcg	tac	acc	acc	atc	aag	gac	att	gaa	ctt	720
Glu	Ala	Ala	Arg	Asp	Asn	Ala	Tyr	Thr	Thr	Ile	Lys	Asp	Ile	Glu	Leu	
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 Arg Ile Ser Ile
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Phe	Phe	Leu 35	Val	Asp	Gly	Glu	Thr 40	Val	Val	Pro	Leu	Leu 45	Pro	Ala	Gln
Asp 50	His	Lys	Arg	Ala	Tyr	Asp 55	Asn	Asp	Glu	Gly	Pro 60	Asn	Thr	Gly	Gly
Met 65	Gly	Ala	Tyr	Ala	Pro 70	Leu	Pro	Trp	Leu	Pro 75	Glu	Asp	Gly	Val	Gln 80
Arg	Ile	Val	Asp	Glu 85	Val	Cys	Val	Pro	Val 90	Ala	Arg	Glu	Met	Val 95	Ala
Arg	Gly	Cys	Ala 100	Tyr	Ser	Gly	Leu	Leu 105	Tyr	Ala	Gly	Ile	Ala 110	Trp	Gly
Ala	Glu	Gly 115	Pro	Ala	Val	Val	Glu	Phe	Asn	Cys	Arg	Phe	Gly	Asp	Pro
Glu 130	Thr	Gln	Ala	Val	Leu	Ala 135	Leu	Leu	Lys	Thr	Pro 140	Leu	Ala	Val	Leu
Leu 145	Asn	Ala	Val	Ala	Thr 150	Gly	Thr	Leu	Ala	Glu 155	Gln	Pro	Ala	Leu	Glu 160
Trp	Glu	Asp	Ala	Tyr 165	Ala	Leu	Thr	Val	Val 170	Leu	Ala	Ser	Tyr	Asn 175	Tyr
Pro	Glu	Ala	Pro 180	Arg	Thr	Gly	Asp	Val 185	Ile	Arg	Asn	Ala	Asp 190	Ala	Asp
Asn	Val	Leu 195	His	Ala	Gly	Thr	Ala 200	Leu	Asn	Ala	Glu	Gly 205	Glu	Leu	Val
Ser 210	Ala	Gly	Gly	Arg	Val	Leu 215	Asn	Val	Ile	Gly	Val 220	Gly	Glu	Thr	Leu
Glu 225	Ala	Ala	Arg	Asp	Asn 230	Ala	Tyr	Thr	Thr	Ile 235	Lys	Asp	Ile	Glu	Leu 240

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 245 250 255

Arg Ile Ser Ile
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<211> 714

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXA02623

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 Val Asn Ser Asp Ser
 1 5

acg acc acc att gtc gtg cta gct tcc gga aca ggc acc ctc ctt cag 163
 Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr Gly Thr Leu Leu Gln
 10 15 20

tca ctc att gaa gcg caa ggt acc tat tcg atc gtg ggc gtt gtc tct 211
 Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile Val Gly Val Val Ser
 25 30 35

gac gtc gaa tgc cct gca ctt tcc aga gcc gca gat gca ggt att gat 259
 Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala Asp Ala Gly Ile Asp
 40 45 50

act gca gtt gtt ccg ctt gga aaa gat cgt gca cag tgg aac cac gag 307
 Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala Gln Trp Asn His Glu
 55 60 65

ctt gca gac gca gtt gca gta agc gac cca gat ttg gtg gtc tct gcg 355
 Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp Leu Val Val Ser Ala
 70 75 80 85

gga ttc atg aaa att ttg ggc gaa ggt ttc ctc tca agg ttc ccg tcc 403
 Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu Ser Arg Phe Pro Ser
 90 95 100

cgc atc atc aac acc cac cca gct tta ttg cct tct ttc cct ggt gcc 451
 Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro Ser Phe Pro Gly Ala
 105 110 115

cac gcg gtt cgc gat gct ttg gca tac ggt gtg aaa gtg tca ggt tcg 499
 His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val Lys Val Ser Gly Ser
 120 125 130

aca gtt cac ctt gtc gat gct ggt gtg gat acc ggc cca att att gct 547
 Thr Val His Leu Val Asp Ala Gly Val Asp Thr Gly Pro Ile Ile Ala
 135 140 145

caa cga gca gtg ccg gta gaa gtg aat gat gat gaa tcc agc ctg cat 595

Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp Glu Ser Ser Leu His
 150 155 160 165

gaa aga atc aag cag gtt gag cgt aaa ctc att gta gaa gtc ctg aac 643
 Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile Val Glu Val Leu Asn
 170 175 180

agc gtg gaa ttt tcg cgt cag ggt ggc gta caa ctc aac tgg aga ggc 691
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Gly Thr Leu Leu Gln Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile
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 35 40 45

Asp Ala Gly Ile Asp Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala
 50 55 60

Gln Trp Asn His Glu Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp
 65 70 75 80

Leu Val Val Ser Ala Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu
 85 90 95

Ser Arg Phe Pro Ser Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro
 100 105 110

Ser Phe Pro Gly Ala His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val
 115 120 125

Lys Val Ser Gly Ser Thr Val His Leu Val Asp Ala Gly Val Asp Thr
 130 135 140

Gly Pro Ile Ile Ala Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp
 145 150 155 160

Glu Ser Ser Leu His Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile
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Val Glu Val Leu Asn Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln
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Leu Asn Trp Arg Gly
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Met Tyr Ile Pro Glu 1 5																
tcg atc ggc acc cct ttg acc ccc aat gcc acg aaa gtg atg ctg ctg 163																
Ser Ile Gly Thr Pro Leu Thr Pro Asn Ala Thr Lys Val Met Leu Leu 10 15 20																
gga tca gga gaa tta ggc aaa gaa gta gcc atc gct ttc cag cgt ctc 211																
Gly Ser Gly Glu Leu Gly Lys Glu Val Ala Ile Ala Phe Gln Arg Leu 25 30 35																
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Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu His Ala Pro Ala His 40 45 50																
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Gln Val Ala His Phe Ser Tyr Val Ile Asp Met Thr Asp Ala Ala Gln 55 60 65																
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Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp Phe Val Ile Pro Glu 70 75 80 85																
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Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys Ile Glu Glu Glu Gly 90 95 100																
cta gct acc atc gtg ccc act gca cgt gca gcc aag ctg acc atg aac 451																
Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala Lys Leu Thr Met Asn 105 110 115																
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Arg Glu Gly Ile Arg Lys Leu Ala Ala Glu Glu Leu Gly Leu Pro Thr 120 125 130																
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Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu Phe Ser Ala Ala Ala 135 140 145																
gaa aag ctt ggt tac ccc aac gtg gtg aaa cca gtg atg agt tct tcc 595																
Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro Val Met Ser Ser Ser 150 155 160 165																
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Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp Asp Leu Gln Ala Ala 170 175 180																
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Val	Glu	Ala	Phe	Val	Glu	Phe	Asp	Tyr	Glu	Ile	Thr	Leu	Leu	Thr	Val		
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agg	tcc	atc	gat	ccc	acc	acc	tct	aag	cct	gcg	acc	tgg	ttc	tgt	gag	787	
Arg	Ser	Ile	Asp	Pro	Thr	Thr	Ser	Lys	Pro	Ala	Thr	Trp	Phe	Cys	Glu		
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Pro	Ile	Gly	His	Arg	Gln	Glu	Asp	Gly	Asp	Tyr	Val	Glu	Ser	Trp	Gln		
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Pro	Met	Glu	Met	Thr	Pro	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Ser	Val	Ala		
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Leu	Ile	Ser	Pro	Gly	Ala	Ser	Ala	Val	Ile	Tyr	Gly	Gly	Ile	Glu	Ser		
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gaa	ggc	gtg	agc	tac	acc	ggg	ttg	gct	gaa	gcg	ctg	gca	gtg	gct	gaa	1171	
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Thr	Asp	Leu	Arg	Ile	Phe	Ala	Lys	Pro	Glu	Ala	Phe	Thr	Lys	Arg	Arg		
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Met	Gly	Val	Ala	Val	Ser	Thr	Ala	Glu	Asp	Val	Ala	Ala	Ala	Arg	Asp		
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cgc	gcc	act	ttg	gct	gcc	gcg	gcg	atc	aag	gtt	cat	cca	gga	aat	tcc	1315	
Arg	Ala	Thr	Leu	Ala	Ala	Ala	Ala	Ile	Lys	Val	His	Pro	Gly	Asn	Ser		
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Ala	Glu	Ala															

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<212> PRT

<213> Corynebacterium glutamicum

<400> 910

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Ala Phe Gln Arg Leu Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu
      35           40           45

His Ala Pro Ala His Gln Val Ala His Phe Ser Tyr Val Ile Asp Met
      50           55           60

Thr Asp Ala Ala Gln Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp
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Phe Val Ile Pro Glu Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys
      85           90           95

Ile Glu Glu Glu Gly Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala
      100          105          110

Lys Leu Thr Met Asn Arg Glu Gly Ile Arg Lys Leu Ala Ala Glu Glu
      115          120          125

Leu Gly Leu Pro Thr Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu
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Phe Ser Ala Ala Ala Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro
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Val Met Ser Ser Ser Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp
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Asp Leu Gln Ala Ala Trp Asp Tyr Ala Met Ser Gly Ala Arg Val Ala
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Asn Ser Arg Val Ile Val Glu Ala Phe Val Glu Phe Asp Tyr Glu Ile
      195          200          205

Thr Leu Leu Thr Val Arg Ser Ile Asp Pro Thr Thr Ser Lys Pro Ala
      210          215          220

Thr Trp Phe Cys Glu Pro Ile Gly His Arg Gln Glu Asp Gly Asp Tyr
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Val Glu Ser Trp Gln Pro Met Glu Met Thr Pro Arg Ala Leu Glu Asn
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Ala Arg Ser Val Ala Ala Arg Ile Thr Asn Ala Leu Gly Gly Arg Gly
      260          265          270

Val Phe Gly Val Glu Leu Phe Val Ser Gly Asp Asp Val Tyr Phe Ser
      275          280          285

Glu Val Ser Pro Arg Pro His Asp Thr Gly Leu Val Thr Leu Ala Thr
      290          295          300

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Gln Arg Phe Ser Glu Phe Glu Leu His Ala Lys Ala Ile Leu Gly Leu
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 Pro Val Asp Val Thr Leu Ile Ser Pro Gly Ala Ser Ala Val Ile Tyr
 325 330 335
 Gly Gly Ile Glu Ser Glu Gly Val Ser Tyr Thr Gly Leu Ala Glu Ala
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 Leu Ala Val Ala Glu Thr Asp Leu Arg Ile Phe Ala Lys Pro Glu Ala
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 Met Ser Thr Phe Val
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 aat gac acc gtc gaa gac gca atc aag acc cct gag ctg gat cag cca 163
 Asn Asp Thr Val Glu Asp Ala Ile Lys Thr Pro Glu Leu Asp Gln Pro
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 ttt gag gct ctt ggt ctg aaa gac gac gag tac gcg cgc atc aag gaa 211
 Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr Ala Arg Ile Lys Glu
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 atc ctt ggc cgc cgc cca acc gac gcc gag ctg acc gtt tac tcc gtc 259
 Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu Thr Val Tyr Ser Val
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 atg tgg tcg gag cac tgc tcc tac aag tcc tcc aag gtt cac ctg cgt 307
 Met Trp Ser Glu His Cys Ser Tyr Lys Ser Ser Lys Val His Leu Arg
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 tac ttc ggt gaa acc acc act gag gaa atg gct tcc aag att ctt gcc 355
 Tyr Phe Gly Glu Thr Thr Glu Glu Met Ala Ser Lys Ile Leu Ala
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 ggc atc ggc gag aac gct ggt gtg gtc gac atc gga gac ggc aac gcc 403

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Val	Thr	Phe	Arg	Val	Glu	Ser	His	Asn	His	Pro	Ser	Phe	Val	Glu	Pro		
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His	Gln	Gly	Ala	Ala	Thr	Gly	Val	Gly	Gly	Ile	Val	Arg	Asp	Ile	Met		
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gct	atg	ggc	gca	cgc	cca	atc	gct	gtg	atg	gat	cag	ctg	cgt	ttc	ggc	547	
Ala	Met	Gly	Ala	Arg	Pro	Ile	Ala	Val	Met	Asp	Gln	Leu	Arg	Phe	Gly		
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Ala	Leu	Asp	Asn	Pro	Asp	Thr	Gln	Arg	Val	Phe	Pro	Gly	Val	Val	Asp		
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Gly	Ile	Ser	His	Tyr	Gly	Asn	Cys	Leu	Gly	Leu	Pro	Asn	Ile	Gly	Gly		
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gaa	acc	gtc	ttc	gac	gat	tcc	tac	gca	ggc	aac	cca	ctg	gtc	aac	gca	691	
Glu	Thr	Val	Phe	Asp	Asp	Ser	Tyr	Ala	Gly	Asn	Pro	Leu	Val	Asn	Ala		
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Leu	Cys	Val	Gly	Thr	Leu	Lys	Val	Glu	Asp	Leu	Lys	Leu	Ala	Phe	Ala		
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Ser	Gly	Thr	Gly	Asn	Lys	Val	Ile	Leu	Phe	Gly	Ser	Arg	Thr	Gly	Leu		
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gat	ggc	atc	ggc	ggc	gtg	tcc	gtc	ctg	ggc	tcc	gca	tcc	ttc	gaa	gaa	835	
Asp	Gly	Ile	Gly	Gly	Val	Ser	Val	Leu	Gly	Ser	Ala	Ser	Phe	Glu	Glu		
	230				235				240					245			
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Gly	Glu	Glu	Arg	Lys	Leu	Pro	Ala	Val	Gln	Val	Gly	Asp	Pro	Phe	Ala		
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Glu	Lys	Val	Leu	Ile	Glu	Cys	Cys	Leu	Glu	Leu	Tyr	Lys	Ala	Gly	Val		
			265					270					275				
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Val	Val	Gly	Ile	Gln	Asp	Leu	Gly	Gly	Gly	Gly	Leu	Ala	Cys	Ala	Thr		
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Asn	Val	Pro	Leu	Arg	Ala	Glu	Asn	Met	Ser	Ala	Ala	Glu	Ile	Leu	Ala		
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Ser	Glu	Ser	Gln	Glu	Arg	Met	Cys	Ala	Val	Val	Thr	Pro	Glu	Asn	Val		

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Ile	Gly	Glu	Val	Thr	Asp	Glu	Lys	Asp	Arg	Tyr	Val	Val	Val	His	Asn				
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ggc	gaa	gtt	gtt	atc	gac	gca	cct	cca	tca	acc	atc	gat	gaa	ggc	cct	1267			
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375				380				385											
gtc	tac	aac	cgc	cca	gtt	gct	cgc	cct	gag	aac	cag	gac	gaa	ctg	cag	1315			
Val	Tyr	Asn	Arg	Pro	Val	Ala	Arg	Pro	Glu	Asn	Gln	Asp	Glu	Leu	Gln				
390				395				400				405							
ctc	gaa	ggc	gag	atc	gct	cgc	cca	gtc	gac	gtt	gaa	gag	atc	aag	gct	1363			
Leu	Glu	Gly	Glu	Ile	Ala	Arg	Pro	Val	Asp	Val	Glu	Glu	Ile	Lys	Ala				
410				415				420											
gct	tgg	ctg	aag	ctt	gtc	gct	tca	cca	gca	ctt	gca	tcc	cgc	gcg	ttt	1411			
Ala	Trp	Leu	Lys	Leu	Val	Ala	Ser	Pro	Ala	Leu	Ala	Ser	Arg	Ala	Phe				
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Ile	Thr	Glu	Gln	Tyr	Asp	Arg	Tyr	Val	Arg	Gly	Asn	Thr	Val	Gln	Ala				
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aag	aac	gcc	aat	gct	ggc	gtc	ttg	cgt	atc	gac	gaa	gag	acc	aac	cgt	1507			
Lys	Asn	Ala	Asn	Ala	Gly	Val	Leu	Arg	Ile	Asp	Glu	Glu	Thr	Asn	Arg				
455				460				465											
ggc	gtt	gcg	atc	tcc	gcc	gac	gca	tcc	ggc	cgt	tac	acc	aag	ctc	gag	1555			
Gly	Val	Ala	Ile	Ser	Ala	Asp	Ala	Ser	Gly	Arg	Tyr	Thr	Lys	Leu	Glu				
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Pro	Asn	Thr	Gly	Ala	Gln	Leu	Ala	Leu	Ala	Glu	Ala	Tyr	Arg	Asn	Val				
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Val	Ser	Thr	Gly	Ala	Arg	Pro	Val	Ala	Val	Thr	Asn	Cys	Leu	Asn	Phe				
505				510				515											
ggc	tcc	cca	gaa	aac	gct	ggc	gtt	atg	tgg	cag	ttc	aag	gaa	gca	gtc	1699			
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Gly	Asn	Val	Ser	Phe	Tyr	Asn	Gln	Thr	Gly	Asp	Glu	Pro	Ile	Leu	Pro				
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acc	cca	gtc	gtg	ggc	gtt	ttg	gga	gtc	ttg	gac	aac	gtc	gag	cag	agc	1843			
Thr	Pro	Val	Val	Gly	Val	Leu	Gly	Val	Leu	Asp	Asn	Val	Glu	Gln	Ser				
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atc ggc aac gtc ctc cca tcc gag gac aac gat ctc tac ctc ctg ggt 1891
 Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu Leu Gly
 585 590 595

gag acc ttc gat gag ttc ggt ggc tcc atc tgg cag cag gtt tct ggc 1939
 Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val Ser Gly
 600 605 610

gct ggc ctc aac ggt ctg cca cca gta gtt gac ctg ctc aac gag cag 1987
 Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn Glu Gln
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cgt ctt gca gac ctg ttc gtc ggt tct gat ctg ttt gct gca tcc cac 2035
 Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala Ser His
 630 635 640 645

gat ctg tct gag ggc ggc ctt ggc cag acc ctc gca gag ctt gcg atc 2083
 Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu Ala Ile
 650 655 660

cac cag aaa aag gga atg gat gtt gat ctc tcc cag atc cac cca tcc 2131
 His Gln Lys Lys Gly Met Asp Val Asp Leu Ser Gln Ile His Pro Ser
 665 670 675

ctg ttc acc tca ctg ttt gct gag tcc gct tcc cgc atc gtg gtt gca 2179
 Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser Arg Ile Val Val Ala
 680 685 690

acc aac cgc ggc gaa gag ttg gaa aag cgc gca gca gag ctg ggt gtt 2227
 Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala Ala Glu Leu Gly Val
 695 700 705

cca gtg ttc aag ctg ggc tgc acc aac gat tca gcc gtc atc gct gtc 2275
 Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser Ala Val Ile Ala Val
 710 715 720 725

aag ggc gca gac gtt gag ttc act gtt tcc gtg gag gaa ctc cgc gaa 2323
 Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val Glu Glu Leu Arg Glu
 730 735 740

gca tgg acc aac act ttg cct gag gcc ttc ggt cac gca gtt gga gct 2371
 Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly His Ala Val Gly Ala
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<400> 912

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 35 40 45
 Thr Val Tyr Ser Val Met Trp Ser Glu His Cys Ser Tyr Lys Ser Ser
 50 55 60
 Lys Val His Leu Arg Tyr Phe Gly Glu Thr Thr Thr Glu Glu Met Ala
 65 70 75 80
 Ser Lys Ile Leu Ala Gly Ile Gly Glu Asn Ala Gly Val Val Asp Ile
 85 90 95
 Gly Asp Gly Asn Ala Val Thr Phe Arg Val Glu Ser His Asn His Pro
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 Ser Phe Val Glu Pro His Gln Gly Ala Ala Thr Gly Val Gly Gly Ile
 115 120 125
 Val Arg Asp Ile Met Ala Met Gly Ala Arg Pro Ile Ala Val Met Asp
 130 135 140
 Gln Leu Arg Phe Gly Ala Leu Asp Asn Pro Asp Thr Gln Arg Val Phe
 145 150 155 160
 Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu
 165 170 175
 Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn
 180 185 190
 Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu
 195 200 205
 Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly
 210 215 220
 Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser
 225 230 235 240
 Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val
 245 250 255
 Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu
 260 265 270
 Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly
 275 280 285
 Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met
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 Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala
 305 310 315 320
 Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val
 325 330 335
 Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp
 340 345 350

Val Thr Cys Ala Glu Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr
 355 360 365
 Val Val Val His Asn Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr
 370 375 380
 Ile Asp Glu Gly Pro Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn
 385 390 395 400
 Gln Asp Glu Leu Gln Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val
 405 410 415
 Glu Glu Ile Lys Ala Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu
 420 425 430
 Ala Ser Arg Ala Phe Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly
 435 440 445
 Asn Thr Val Gln Ala Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp
 450 455 460
 Glu Glu Thr Asn Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg
 465 470 475 480
 Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu
 485 490 495
 Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr
 500 505 510
 Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln
 515 520 525
 Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly
 530 535 540
 Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp
 545 550 555 560
 Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp
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 Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp
 580 585 590
 Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp
 595 600 605
 Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp
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 Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu
 625 630 635 640
 Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu
 645 650 655
 Ala Glu Leu Ala Ile His Gln Lys Lys Gly Met Asp Val Asp Leu Ser
 660 665 670
 Gln Ile His Pro Ser Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser

675					680					685					
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690						695					700				
Ala	Glu	Leu	Gly	Val	Pro	Val	Phe	Lys	Leu	Gly	Cys	Thr	Asn	Asp	Ser
705					710					715					720
Ala	Val	Ile	Ala	Val	Lys	Gly	Ala	Asp	Val	Glu	Phe	Thr	Val	Ser	Val
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Glu	Glu	Leu	Arg	Glu	Ala	Trp	Thr	Asn	Thr	Leu	Pro	Glu	Ala	Phe	Gly
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 Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu
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cca aac atc ggt ggc gaa acc gtc ttc gac gat tcc tac gca ggt aac 155
 Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn
 20 25 30

cca ctg gtc aac gca ctg tgc gtg ggt acc ctc aag gtg gaa gac ctc 203
 Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu
 35 40 45 50

aag ctt gca ttc gca tcc ggc acc ggc aac aag gtg atc ctg ttc ggt 251
 Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly
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 Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser
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gca tcc ttc gaa gaa ggc gaa gag cgc aag ctc cca gct gtt cag gtt 347
 Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val
 85 90 95

ggc gat cct ttc gca gag aag gta ctc atc gag tgc tgc ctc gag ctg 395
 Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu
 100 105 110

tac aag gct ggc gtc gtg gtc ggt att cag gac ctc ggt ggc ggc gga 443
 Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly
 115 120 125 130

ctt gcg tgt gca acc tct gag ctg gca gcc gca ggc gac ggc ggc atg 491
 Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Gly Asp Gly Gly Met
 135 140 145

cgc gtc aac cta gac aac gtc cca ctg cgc gca gag aac atg tct gca 539
 Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala
 150 155 160

gct gaa atc ctg gct tcc gag tcc cag gag cgc atg tgt gct gtt gtc 587
 Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val
 165 170 175

acc cct gaa aac gtt gag cgt ttc ctc gag atc tgt gca aag tgg gat 635
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gtc 638
 Val
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<210> 914

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Gly Asn Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu
 35 40 45

Asp Leu Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu
 50 55 60

Phe Gly Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu
 65 70 75 80

Gly Ser Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val
 85 90 95

Gln Val Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu
 100 105 110

Glu Leu Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly
 115 120 125

Gly Gly Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly
 130 135 140

Gly Met Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met
 145 150 155 160

Ser Ala Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala
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Val Val Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys
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Trp Asp Val
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Ser Ala Ala Thr Pro Phe Lys Gln Lys Asn Ala Asn Ala Gly Val Leu	
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cgt atc gac gaa gag acc anc cgt ggc gtt gcg atc tcc gcc gac gca	148
Arg Ile Asp Glu Glu Thr Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala	
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Ser Gly Arg Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala	
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ctg gct gag gct tac cgc aac gtg gtc tcc acc ggt gca cgc cca gtg	244
Leu Ala Glu Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val	
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gct gtc acc aac tgc ctg aac ttc ggt tcc cca gaa aac gct ggt gtt	292
Ala Val Thr Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val	
75 80 85 90	
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Met Trp Gln Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys	
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Leu Leu Gly Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln	
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act ggt gac gag ccc atc ctg cca acc cca gtc gtg ggt gtt ttg gga	436
Thr Gly Asp Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly	
125 130 135	
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Val Leu Asp Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu	
140 145 150	

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 Asp Asn Asp Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly
 155 160 165 170

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 175 180 185

gta gtt gac ctg ctc aac gag cag cgt ctt gca gac ctg ttc gtc ggt 628
 Val Val Asp Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly
 190 195 200

tct gat ctg ttt gct gca tcc cac gat ctg tct gag ggc ggc ctt ggc 676
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<210> 916

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<213> Corynebacterium glutamicum

<400> 916

Val Tyr His Arg Ala Val Leu Asn Ala Thr Ser Ala Ala Thr Pro Phe
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Lys Gln Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr
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Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys
 35 40 45

Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg
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Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr Asn Cys Leu
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Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu
 85 90 95

Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val
 100 105 110

Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile
 115 120 125

Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu
 130 135 140

Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu
 145 150 155 160

Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val
 165 170 175

Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn

	180		185		190
Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala					
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Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu					
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ccc gct tcc cgc atc gtg gtt gca acc aac cgc ggc gaa gag ttg gaa	96
Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu	
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aag cgc gca gca gag ctg ggt gtt cca gtg ttc aag ctg ggc tgc acc	144
Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr	
35 40 45	
aac gat tca gcc gtc atc gct gtc aag ggc gca gac gtt gag ttc act	192
Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr	
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gtt tcc gtg gag gaa ctc cgc gaa gca tgg acc aac act ttg cct gag	240
Val Ser Val Glu Glu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu	
65 70 75 80	
gcc ttc ggt cac gca gtt gga gct aac gca gta gtt gca taattttctg	289
Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala	
85 90	
ctgtgaagcc ggg	302

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20 25 30

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ggt gtc att acc ttc cca ggc acc ctt gac gat gta gat gca gca cgc																	163					
Gly	Val	Ile	Thr	Phe	Pro	Gly	Thr	Leu	Asp	Asp	Val	Asp	Ala	Ala	Arg							
																	10				20	
gct gct cgc atc gca ggt gca gaa gta atc agc ctg tgg cac gct gac																	211					
Ala	Ala	Arg	Ile	Ala	Gly	Ala	Glu	Val	Ile	Ser	Leu	Trp	His	Ala	Asp							
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Glu	Asp	Leu	Lys	Gly	Val	Asp	Ala	Val	Val	Val	Pro	Gly	Gly	Phe	Ser							
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tac gcc gat tac ctg cgc acc ggt gca atc tct gca ctg gcg cca gta																	307					
Tyr	Gly	Asp	Tyr	Leu	Arg	Thr	Gly	Ala	Ile	Ser	Ala	Leu	Ala	Pro	Val							
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Met	Gln	Ser	Val	Ile	Glu	Gln	Ala	Gly	Lys	Gly	Met	Pro	Val	Leu	Gly							
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att tgc aac ggc ttc cag atc ctc acc gaa gca cgc ctg ctt cca ggc																	403					
Ile	Cys	Asn	Gly	Phe	Gln	Ile	Leu	Thr	Glu	Ala	Arg	Leu	Leu	Pro	Gly							
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gcg ctg acc cgc aac aag ggt ctg cac ttt cac tgt gta gac gca cac																	451					
Ala	Leu	Thr	Arg	Asn	Lys	Gly	Leu	His	Phe	His	Cys	Val	Asp	Ala	His							
																	105				115	
ctc gtt gta gag aac aac acc act gca tgg acc aac act ttg gaa aag																	499					
Leu	Val	Val	Glu	Asn	Asn	Thr	Thr	Ala	Trp	Thr	Asn	Thr	Leu	Glu	Lys							

120	125	130	
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gca gac gca gag acc atc gcc cag ctt gag ggt gaa ggc cgc gtg gtg Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly Glu Gly Arg Val Val 150 155 160 165			595
ttc cgt tac acc gat aac ttc aac ggt tcc gtc aac gat atc gcc ggt Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val Asn Asp Ile Ala Gly 170 175 180			643
atc act aat gaa act ggt cgc atc gtc ggt ctc atg ccg cac ccg gaa Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu Met Pro His Pro Glu 185 190 195			691
cat gcc gtc gaa aag cta acc ggc cca tct att gat ggc ctg gag ctg His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile Asp Gly Leu Glu Leu 200 205 210			739
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Pro Gly Gly Phe Ser Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser 50 55 60			
Ala Leu Ala Pro Val Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly 65 70 75 80			
Met Pro Val Leu Gly Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala 85 90 95			
Arg Leu Leu Pro Gly Ala Leu Thr Arg Asn Lys Gly Leu His Phe His 100 105 110			
Cys Val Asp Ala His Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr 115 120 125			
Asn Thr Leu Glu Lys Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly 130 135 140			

Glu Gly Arg Phe Gln Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly
 145 150 155 160
 Glu Gly Arg Val Val Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val
 165 170 175
 Asn Asp Ile Ala Gly Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu
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 Asp Gly Leu Glu Leu Phe Leu Ser Ala Val Gly Thr Ile Ala Ala
 210 215 220

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 Met Arg Pro Glu Leu
 1 5
 tcc cag tac aag cac ctg tcg gca ggc aag gtc cgt gag atc tac gag 163
 Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val Arg Glu Ile Tyr Glu
 10 15 20
 atc gac gac aag cac atc ctc atg gtg gct tcc gat cgt atc tct gca 211
 Ile Asp Asp Lys His Ile Leu Met Val Ala Ser Asp Arg Ile Ser Ala
 25 30 35
 tac gat ttc atc ctc gat acc gaa att cca gac aag ggt cga gtg ctc 259
 Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp Lys Gly Arg Val Leu
 40 45 50
 act gcg atg agc cag ttc ttc ttc gac acc atc gat ttt cct aat cac 307
 Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile Asp Phe Pro Asn His
 55 60 65
 ctt gca ggt ccc gct gat gat cca cgt atc cca gaa gaa gtt ttg gga 355
 Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro Glu Glu Val Leu Gly
 70 75 80 85
 cga gca atg gtg tgc aag aag ctc aac atg ctt cct ttt gaa tgc gtg 403
 Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu Pro Phe Glu Cys Val
 90 95 100
 gtt cgt gga tac ctc act ggc tct gga ctt gtt gaa tac aag cag acc 451
 Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val Glu Tyr Lys Gln Thr
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Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly Leu Val Glu Ser Ser
      120                      125                      130

cag ctg cct gag cca atc ttt acc cca gcc acc aag gct gac atc ggc 547
Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr Lys Ala Asp Ile Gly
      135                      140                      145

gac cac gac atc aat gtc tcc ttt gac gtt gtt gaa gaa cgt ctc ggc 595
Asp His Asp Ile Asn Val Ser Phe Asp Val Val Glu Glu Arg Leu Gly
      150                      155                      160                      165

gaa gct cgt gcg aac cag ttg cgc gat gcc tct att gct att tac aag 643
Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser Ile Ala Ile Tyr Lys
      170                      175                      180

gct gct gct gag atc gcc cgt gac cgt ggc gtc atc ctt gcc gac acc 691
Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val Ile Leu Ala Asp Thr
      185                      190                      195

aaa ttt gag ttc ggc atc gat gaa gat ggc acc ctc gtg ctt ggt gat 739
Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr Leu Val Leu Gly Asp
      200                      205                      210

gaa gtc ctt acc cca gat tcc tcc cgc tac tgg cct ttg gaa ggc tat 787
Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp Pro Leu Glu Gly Tyr
      215                      220                      225

gaa gca gga tct gtg caa cca agc ttt gat aag caa ttc gtg cgc aac 835
Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys Gln Phe Val Arg Asn
      230                      235                      240                      245

tgg ctc acc ggc cct aaa tct ggc tgg gac aag gat tcc ggc ttg gag 883
Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys Asp Ser Gly Leu Glu
      250                      255                      260

cca cca gct ctg cca ggt tcc gtt gtt gag gca acc cgc gag cgc tac 931
Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala Thr Arg Glu Arg Tyr
      265                      270                      275

atc gag gcc tac gag ctg att tct ggt cag aag ttc tgc cag tgg att 979
Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys Phe Cys Gln Trp Ile
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Gly Ser Cys Val
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<211> 297

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<400> 922

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      20           25           30

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Asp Arg Ile Ser Ala Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp
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 Lys Gly Arg Val Leu Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile
 50 55 60
 Asp Phe Pro Asn His Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro
 65 70 75 80
 Glu Glu Val Leu Gly Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu
 85 90 95
 Pro Phe Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val
 100 105 110
 Glu Tyr Lys Gln Thr Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly
 115 120 125
 Leu Val Glu Ser Ser Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr
 130 135 140
 Lys Ala Asp Ile Gly Asp His Asp Ile Asn Val Ser Phe Asp Val Val
 145 150 155 160
 Glu Glu Arg Leu Gly Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser
 165 170 175
 Ile Ala Ile Tyr Lys Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val
 180 185 190
 Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr
 195 200 205
 Leu Val Leu Gly Asp Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp
 210 215 220
 Pro Leu Glu Gly Tyr Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys
 225 230 235 240
 Gln Phe Val Arg Asn Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys
 245 250 255
 Asp Ser Gly Leu Glu Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala
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<223> RXN00770

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                Leu Leu Ser Pro Tyr
                1 5

gcg tgg ggg ttg tcc cgc gca ctt tta gac agt tat gtt cct aat aag 163
Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser Tyr Val Pro Asn Lys
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ttc caa acc cca gca gga gaa gcg aag tac acg atg agt gat cac cag 211
Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr Met Ser Asp His Gln
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gac acc acc gcc gaa ggc gtt tca tac gca gca gca gga gtc gac atc 259
Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala Ala Gly Val Asp Ile
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gaa gcc ggc gat cgt gcc gtc gaa ctc ttt gca cca atg gcc aag cgc 307
Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala Pro Met Ala Lys Arg
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gcc acc cgc cca gag gtt ctt ggc aac ctc gga ggc ttc gca gga ctc 355
Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly Gly Phe Ala Gly Leu
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ttt gag ctc gga aaa tac aag aag cca atc ctc gca gca gga tct gac 403
Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu Ala Ala Gly Ser Asp
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gga gtc ggc acc aag ctt gtc atc gcc cag atg atg gac aag cac gac 451
Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met Met Asp Lys His Asp
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acc atc ggc atc gac ctt gtt gca atg tgt gtg gat gac ctc gtt gtc 499
Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val Asp Asp Leu Val Val
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acc ggc gca gag cca ctg ttc ctc cag gac tac atc gcc atc ggc aag 547
Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr Ile Ala Ile Gly Lys
                135 140 145

gtt gtc cca gag cac gtt gct gag atc gtc tcc ggt atc gca gaa ggc 595
Val Val Pro Glu His Val Ala Glu Ile Val Ser Gly Ile Ala Glu Gly
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Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly Glu Thr Ala Glu His
                170 175 180

cca ggt gtt atg gaa cca gac cac tac gat gtc tcc gca act gca gtc 691
Pro Gly Val Met Glu Pro Asp His Tyr Asp Val Ser Ala Thr Ala Val
                185 190 195

ggc gtt gtc gaa gca gat gaa ctg cta gga cca gac cgc gtc cgc gca 739
Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro Asp Arg Val Arg Ala
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 tac tcc ctg gct cgc cac gtc ctc ctg gaa aag gca ggc ctg gcg ctt 835
 Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys Ala Gly Leu Ala Leu
 230 235 240 245
 gac gga cac atc gaa gaa ctc gga cgc acc ctc ggt gaa gaa ctt ctc 883
 Asp Gly His Ile Glu Glu Leu Gly Arg Thr Leu Gly Glu Glu Leu Leu
 250 255 260
 gag cca acc cgc atc tac gcc aag gac tgc ctg gca ctg atc gca gag 931
 Glu Pro Thr Arg Ile Tyr Ala Lys Asp Cys Leu Ala Leu Ile Ala Glu
 265 270 275
 tgc gaa gtt cac acc ttc tgc cac gtc acc ggc ggc ggc ctc gca ggc 979
 Cys Glu Val His Thr Phe Cys His Val Thr Gly Gly Gly Leu Ala Gly
 280 285 290
 aac ctc gag cgg gtt gtc cca gaa ggg ctc gtc gca gaa atg tcc cga 1027
 Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val Ala Glu Met Ser Arg
 295 300 305
 gca act tgg acc cca ggc caa atc ttc cgc acc atc tcc tct gtg ggc 1075
 Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr Ile Ser Ser Val Gly
 310 315 320 325
 aag gtt tcc cgc gaa gaa atg gaa aag acc ttc aac atg ggt gtc ggc 1123
 Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe Asn Met Gly Val Gly
 330 335 340
 atg gtt gca gtc gtt gct gaa aag gac cgc gac cgc gcc ctg gca atg 1171
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 345 350 355
 ctc acc gca cgt cac att gac tgc tgg gaa atc gga acc gta cgc aac 1219
 Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile Gly Thr Val Arg Asn
 360 365 370
 ggt gaa gag gga gag cct cgc gtg atc ctc aac ggc gag cac cct ggc 1267
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<212> PRT

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 Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala
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 65 70 75 80
 Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu
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 Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met
 100 105 110
 Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val
 115 120 125
 Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr
 130 135 140
 Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser
 145 150 155 160
 Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly
 165 170 175
 Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val
 180 185 190
 Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro
 195 200 205
 Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly
 210 215 220
 Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys
 225 230 235 240
 Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Leu
 245 250 255
 Gly Glu Glu Leu Leu Glu Pro Thr Arg Ile Tyr Ala Lys Asp Cys Leu
 260 265 270
 Ala Leu Ile Ala Glu Cys Glu Val His Thr Phe Cys His Val Thr Gly
 275 280 285
 Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val
 290 295 300
 Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr
 305 310 315 320
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 325 330 335
 Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys Asp Arg Asp
 340 345 350
 Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile

355 360 365
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 <223> FRXA00557

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 Ala Lys Tyr Thr Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val
 30 35 40
 tca tac gca gca gca gga gtc gac atc gaa gcc ggc gat cgt gcc gtc 194
 Ser Tyr Ala Ala Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val
 45 50 55 60
 gaa ctc ttt gca cca atg gcc aag cgc gcc acc cgc cca gag gtt ctt 242
 Glu Leu Phe Ala Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu
 65 70 75
 ggc aac ctc gga ggc ttc gca gga ctc ttt gag ctc gga aaa tac aag 290
 Gly Asn Leu Gly Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys
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 aag cca atc ctc gca gca gga tct gac gga gtc ggc acc aag ctt gtc 338
 Lys Pro Ile Leu Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val
 95 100 105
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 Ile Ala Gln Met Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val
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 Ala Met Cys Val Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe
 125 130 135 140
 ctc cag gac tac atc gcc atc ggc aag gtt gtc cca gag cac gtt gct 482
 Leu Gln Asp Tyr Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala
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Glu Ile Val Ser Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala
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 ctg ctc ggt ggc gaa acc gca gaa cac cca ggt gtt atg gaa cca gac 578
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 175 180 185
 cac tac gat gtc tcc gca act gca gtc ggc gtt gtc gaa gca gat gaa 626
 His Tyr Asp Val Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu
 190 195 200
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 Leu Leu Gly Pro Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met
 205 210 215 220
 gct tcc tcc ggt ctg cac tcc aac ggt tac tcc ctg gct cgc cac gtc 722
 Ala Ser Ser Gly Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val
 225 230 235
 ctc ctg gaa aag gca ggc ctg gcg ctt gac gga cac atc gaa gaa ctc 770
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 35 40 45
 Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala
 50 55 60
 Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly
 65 70 75 80
 Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu
 85 90 95
 Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met
 100 105 110
 Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val
 115 120 125
 Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr
 130 135 140

Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser
 145 150 155 160

Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly
 165 170 175

Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val
 180 185 190

Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro
 195 200 205

Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly
 210 215 220

Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys
 225 230 235 240

Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Pro
 245 250 255

Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala
 260 265

<210> 927

<211> 338

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(315)

<223> FRXA00770

<400> 927

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ggg ctc gtc gca gaa atg tcc cga gca act tgg acc cca ggc caa atc	96
Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile	
20 25 30	
ttc cgc acc atc tcc tct gtg ggc aag gtt tcc cgc gaa gaa atg gaa	144
Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu	
35 40 45	
aag acc ttc aac atg ggt gtc ggc atg gtt gca gtc gtt gct gaa aag	192
Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys	
50 55 60	
gac cgc gac cgc gcc ctg gca atg ctc acc gca cgt cac att gac tgc	240
Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys	
65 70 75 80	
tgg gaa atc gga acc gta cgc aac ggt gaa gag gga gag cct cgc gtg	288
Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val	
85 90 95	
atc ctc aac ggc gag cac cct ggc tac taagcccaac tgtctgtct	335

Ile Leu Asn Gly Glu His Pro Gly Tyr
 100 105

aag

338

<210> 928

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 928

Val Thr Gly Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu
 1 5 10 15

Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile
 20 25 30

Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu
 35 40 45

Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys
 50 55 60

Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys
 65 70 75 80

Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val
 85 90 95

Ile Leu Asn Gly Glu His Pro Gly Tyr
 100 105

<210> 929

<211> 1320

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1297)

<223> RXN02345

<400> 929

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aagatcttac attttggtga aggcgttata gttaggactt gtg act tct aca gga 115
 Val Thr Ser Thr Gly
 1 5

aac caa gcc cac gct cca gga atg ccc atc gtc gca gta att ggt gac 163
 Asn Gln Ala His Ala Pro Gly Met Pro Ile Val Ala Val Ile Gly Asp
 10 15 20

ggc caa tta gcc cgc atg atg cag acc tcc gcc atc gaa ctc gga caa 211
 Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala Ile Glu Leu Gly Gln
 25 30 35

tca ctg cga gtt cta gct gga gcg ccg gat tcc tcc gca gct caa gta 259
 Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser Ser Ala Ala Gln Val

40					45					50						
gct	gct	gat	gtt	gtt	ctc	ggc	gat	tac	acc	aac	att	gat	gat	ctg	cgc	307
Ala	Ala	Asp	Val	Val	Leu	Gly	Asp	Tyr	Thr	Asn	Ile	Asp	Asp	Leu	Arg	
	55					60					65					
gtc	gcc	atc	gaa	ggc	gcc	gat	gtg	atg	acc	ttc	gac	cac	gag	cac	gtc	355
Val	Ala	Ile	Glu	Gly	Ala	Asp	Val	Met	Thr	Phe	Asp	His	Glu	His	Val	
	70				75					80					85	
ccc	aac	gaa	cac	ctg	cac	caa	ctc	atc	gca	gaa	ggc	gtc	aac	gtt	cag	403
Pro	Asn	Glu	His	Leu	His	Gln	Leu	Ile	Ala	Glu	Gly	Val	Asn	Val	Gln	
				90					95					100		
cca	cgc	cca	gaa	gcg	ctg	gtc	aac	gca	caa	gac	aaa	ctt	gtc	atg	cgc	451
Pro	Arg	Pro	Glu	Ala	Leu	Val	Asn	Ala	Gln	Asp	Lys	Leu	Val	Met	Arg	
			105					110					115			
aag	cgt	cta	cgt	gaa	ctc	ggc	gca	cca	gtc	cca	cca	ttt	gct	gcc	att	499
Lys	Arg	Leu	Arg	Glu	Leu	Gly	Ala	Pro	Val	Pro	Pro	Phe	Ala	Ala	Ile	
		120					125					130				
gaa	tca	gtc	gaa	gat	gca	gtg	gga	ttc	ttc	gaa	gca	gtt	gat	ggc	caa	547
Glu	Ser	Val	Glu	Asp	Ala	Val	Gly	Phe	Phe	Glu	Ala	Val	Asp	Gly	Gln	
	135					140					145					
gtt	tgc	ctc	aaa	gca	cgc	cgt	ggc	gga	tac	gac	ggc	aag	ggc	gta	tgg	595
Val	Cys	Leu	Lys	Ala	Arg	Arg	Gly	Gly	Tyr	Asp	Gly	Lys	Gly	Val	Trp	
	150				155					160					165	
ttc	cca	gcc	gat	gta	gca	gag	ctt	cag	tcg	ctt	gtg	gca	gag	ctt	ctc	643
Phe	Pro	Ala	Asp	Val	Ala	Glu	Leu	Gln	Ser	Leu	Val	Ala	Glu	Leu	Leu	
				170					175					180		
gac	ggc	ggc	acc	cca	ctc	atg	gca	gaa	aag	aaa	gtt	gcc	ctc	aac	agg	691
Asp	Gly	Gly	Thr	Pro	Leu	Met	Ala	Glu	Lys	Lys	Val	Ala	Leu	Asn	Arg	
			185					190					195			
gaa	ctg	tcc	gcc	atg	gtt	gcc	cgc	acc	cca	agt	gga	gaa	acc	aaa	gcg	739
Glu	Leu	Ser	Ala	Met	Val	Ala	Arg	Thr	Pro	Ser	Gly	Glu	Thr	Lys	Ala	
		200					205					210				
tgg	cca	gtc	gta	gaa	tca	gtg	cag	aag	aac	ggt	gtg	tgt	gca	gaa	gca	787
Trp	Pro	Val	Val	Glu	Ser	Val	Gln	Lys	Asn	Gly	Val	Cys	Ala	Glu	Ala	
	215					220					225					
atc	gct	ccc	gca	cct	gaa	cta	tcc	gca	gaa	ctg	cag	gaa	tcc	acc	aga	835
Ile	Ala	Pro	Ala	Pro	Glu	Leu	Ser	Ala	Glu	Leu	Gln	Glu	Ser	Thr	Arg	
	230				235					240					245	
gga	ttg	gcc	cag	aag	atc	gcc	acg	gaa	ctc	ggc	gtc	act	ggt	gtc	ttg	883
Gly	Leu	Ala	Gln	Lys	Ile	Ala	Thr	Glu	Leu	Gly	Val	Thr	Gly	Val	Leu	
				250					255					260		
gca	gtg	gag	ctt	ttt	gaa	acc	ctc	gac	caa	aac	ggg	cag	cca	gag	atc	931
Ala	Val	Glu	Leu	Phe	Glu	Thr	Leu	Asp	Gln	Asn	Gly	Gln	Pro	Glu	Ile	
			265					270					275			
ttt	gtc	aac	gag	ctc	gcc	atg	cgt	tca	cac	aac	acc	ggc	cac	tgg	act	979
Phe	Val	Asn	Glu	Leu	Ala	Met	Arg	Ser	His	Asn	Thr	Gly	His	Trp	Thr	
		280					285					290				

caa gat ggc tgc gtg acc agc caa ttc gag cag cac ctc cgc gca gtc 1027
 Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His Leu Arg Ala Val
 295 300 305

ctc gac tac cca ctg ggt gct acc gac act ttg gct gat tac acc gtg 1075
 Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala Asp Tyr Thr Val
 310 315 320 325

atg gcc aac gtg ctc ggt gcc gac acc gac cca gag atg ccc atg gca 1123
 Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu Met Pro Met Ala
 330 335 340

acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat gcc aag att cac 1171
 Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp Ala Lys Ile His
 345 350 355

ctc tac ggc aag gga cat cgc ccg gga cga aag att ggc cac gtc aac 1219
 Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile Gly His Val Asn
 360 365 370

atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa gcc ctg gcc tgc 1267
 Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu Ala Leu Ala Cys
 375 380 385

gca tac ttc ctt gtc aac gct cgc tgg gat taggtctttt ctgagcgcta 1317
 Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
 390 395

gca 1320

<210> 930

<211> 399

<212> PRT

<213> Corynebacterium glutamicum

<400> 930

Val Thr Ser Thr Gly Asn Gln Ala His Ala Pro Gly Met Pro Ile Val
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Ala Val Ile Gly Asp Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala
 20 25 30

Ile Glu Leu Gly Gln Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser
 35 40 45

Ser Ala Ala Gln Val Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn
 50 55 60

Ile Asp Asp Leu Arg Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe
 65 70 75 80

Asp His Glu His Val Pro Asn Glu His Leu His Gln Leu Ile Ala Glu
 85 90 95

Gly Val Asn Val Gln Pro Arg Pro Glu Ala Leu Val Asn Ala Gln Asp
 100 105 110

Lys Leu Val Met Arg Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro
 115 120 125

Pro Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu
 130 135 140
 Ala Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp
 145 150 155 160
 Gly Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu
 165 170 175
 Val Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys
 180 185 190
 Val Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser
 195 200 205
 Gly Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly
 210 215 220
 Val Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu
 225 230 235 240
 Gln Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly
 245 250 255
 Val Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn
 260 265 270
 Gly Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn
 275 280 285
 Thr Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln
 290 295 300
 His Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu
 305 310 315 320
 Ala Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro
 325 330 335
 Glu Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro
 340 345 350
 Asp Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys
 355 360 365
 Ile Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala
 370 375 380
 Glu Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
 385 390 395

<210> 931

<211> 833

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(810)

<223> FRXA02345

<400> 931

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ggt gat ggc caa gtt tgc ctc aaa gca cgc cgt ggc gga tac gac ggc	96
Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly	
20 25 30	
aag ggc gta tgg ttc cca gcc gat gta gca gag ctt cag tcg ctt gtg	144
Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val	
35 40 45	
gca gag ctt ctc gac ggc ggc acc cca ctc atg gca gaa aag aaa gtt	192
Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val	
50 55 60	
gcc ctc aac agg gaa ctg tcc gcc atg gtt gcc cgc acc cca agt gga	240
Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly	
65 70 75 80	
gaa acc aaa gcg tgg cca gtc gta gaa tca gtg cag aag aac ggt gtg	288
Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val	
85 90 95	
tgt gca gaa gca atc gct ccc gca cct gaa cta tcc gca gaa ctg cag	336
Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln	
100 105 110	
gaa tcc acc aga gga ttg gcc cag aag atc gcc acg gaa ctc ggc gtc	384
Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val	
115 120 125	
act ggt gtc ttg gca gtg gag ctt ttt gaa acc ctc gac caa aac ggg	432
Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly	
130 135 140	
cag cca gag atc ttt gtc aac gag ctc gcc atg cgt tca cac aac acc	480
Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr	
145 150 155 160	
ggc cac tgg act caa gat ggc tgc gtg acc agc caa ttc gag cag cac	528
Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His	
165 170 175	
ctc cgc gca gtc ctc gac tac cca ctg ggt gct acc gac act ttg gct	576
Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala	
180 185 190	
gat tac acc gtg atg gcc aac gtg ctc ggt gcc gac acc gac cca gag	624
Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu	
195 200 205	
atg ccc atg gca acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat	672
Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp	
210 215 220	
gcc aag att cac ctc tac ggc aag gga cat cgc ccg gga cga aag att	720
Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile	

225 230 235 240
 ggc cac gtc aac atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa 768
 Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu
 245 250 255
 gcc ctg gcc tgc gca tac ttc ctt gtc aac gct cgc tgg gat 810
 Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
 260 265 270
 taggtctttt ctgagcgcta gca 833

<210> 932
 <211> 270
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 932
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 1 5 10 15
 Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly
 20 25 30
 Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val
 35 40 45
 Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val
 50 55 60
 Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly
 65 70 75 80
 Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val
 85 90 95
 Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln
 100 105 110
 Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val
 115 120 125
 Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly
 130 135 140
 Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr
 145 150 155 160
 Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His
 165 170 175
 Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala
 180 185 190
 Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu
 195 200 205
 Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp
 210 215 220

Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile
225 230 235 240

Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu
245 250 255

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
260 265 270

<210> 933

<211> 618

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(595)

<223> RXN02350

<400> 933

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ataaacccgat acgtactttt cgcgcttaag gagaatttca gtg ggt cct cta gtt 115
Val Gly Pro Leu Val
1 5

ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct 163
Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala
10 15 20

gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc 211
Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val
25 30 35

tct gca cac cgc acc cca gag aag atg ctc aac tac gca aag act gca 259
Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn Tyr Ala Lys Thr Ala
40 45 50

cat gag cgc ggc atc aag acg atc atc gcg tgt gct ggc ggc gct gca 307
His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys Ala Gly Gly Ala Ala
55 60 65

cac ctg cca ggc atg gtg gct gca gca act cca ctt cca gtc atc ggt 355
His Leu Pro Gly Met Val Ala Ala Ala Thr Pro Leu Pro Val Ile Gly
70 75 80 85

gtt cca cgc gca ttg aag gat ctc gac ggt ttg gat tcc ttg ctg tcc 403
Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu Asp Ser Leu Leu Ser
90 95 100

atc gtc cag atg cca ggc ggc gtt cca gtc gcc act gtc tcc atc ggt 451
Ile Val Gln Met Pro Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly
105 110 115

ggc gcg aag aat gca ggc cta ctt gcc gtt cgt att ctc ggt gct ggt 499
Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly
120 125 130

gat cct tct ttg gtc acg aag atg gcc gat tac caa gag aat atg gcg 547
Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala

135 140 145

aag gaa gtt gaa gcc aag gac gaa gca ctg aag aag cgc ttg ctc ggc 595
 Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly
 150 155 160 165

taatgaatcc gatcgtggtg ctg 618

<210> 934
 <211> 165
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 934
 Val Gly Pro Leu Val Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp
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 Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe
 20 25 30
 Glu Val Gly Val Val Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn
 35 40 45
 Tyr Ala Lys Thr Ala His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys
 50 55 60
 Ala Gly Gly Ala Ala His Leu Pro Gly Met Val Ala Ala Ala Thr Pro
 65 70 75 80
 Leu Pro Val Ile Gly Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu
 85 90 95
 Asp Ser Leu Leu Ser Ile Val Gln Met Pro Gly Gly Val Pro Val Ala
 100 105 110
 Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg
 115 120 125
 Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr
 130 135 140
 Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys
 145 150 155 160
 Lys Arg Leu Leu Gly
 165

<210> 935
 <211> 223
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(223)
 <223> FRXA02346

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ataaaccgat acgtaacttt cgcgcttaag gagaatttca gtg ggt cct cta gtt 115
 Val Gly Pro Leu Val
 1 5

ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct 163
 Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala
 10 15 20

gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc 211
 Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val
 25 30 35

tct gca cac cgc 223
 Ser Ala His Arg
 40

<210> 936

<211> 41

<212> PRT

<213> Corynebacterium glutamicum

<400> 936

Val Gly Pro Leu Val Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp
 1 5 10 15

Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe
 20 25 30

Glu Val Gly Val Val Ser Ala His Arg
 35 40

<210> 937

<211> 252

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (20)..(229)

<223> FRXA02350

<400> 937

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 Leu Asp Ser Leu Leu Ser Ile Val Gln Met Pro
 1 5 10

ggc ggc gtt cca gtc gcc act gtc tcc atc ggt ggc gcg aag aat gca 100
 Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala
 15 20 25

ggc cta ctt gcc gtt cgt att ctc ggt gct ggt gat cct tct ttg gtc 148
 Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val
 30 35 40

acg aag atg gcc gat tac caa gag aat atg gcg aag gaa gtt gaa gcc 196
 Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala
 45 50 55

aag gac gaa gca ctg aag aag cgc ttg ctc ggc taatgaatcc gatcgtgggtg 249
 Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly
 60 65 70

ctg 252

<210> 938
 <211> 70
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 938
 Leu Asp Ser Leu Leu Ser Ile Val Gln Met Pro Gly Gly Val Pro Val
 1 5 10 15
 Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val
 20 25 30
 Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp
 35 40 45
 Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu
 50 55 60
 Lys Lys Arg Leu Leu Gly
 65 70

<210> 939
 <211> 999
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(976)
 <223> RXA01087

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 Met Gln Thr Leu Ala
 1 5
 gct att gtt cgt gcc acg aag caa cct ttt gag atc acc acc att gat 163
 Ala Ile Val Arg Ala Thr Lys Gln Pro Phe Glu Ile Thr Thr Ile Asp
 10 15 20
 ctg gat gca cca cga cca gat gaa gtt caa atc cgt gtt att gct gcc 211
 Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile Arg Val Ile Ala Ala
 25 30 35
 gga gtg cgc cac act gac gca att gtt cgt gat cag att tac cca act 259
 Gly Val Arg His Thr Asp Ala Ile Val Arg Asp Gln Ile Tyr Pro Thr
 40 45 50
 ttt ctt ccc gca gtt ttc ggc cac gaa ggc gcc gga gta gtt gtc gcc 307
 Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala Gly Val Val Val Ala
 55 60 65

gtg ggt tct gca gtc acc tcg gtg aaa cca gat gac aag gta gtg ctg	355
Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp Asp Lys Val Val Leu	
70 75 80 85	
gga ttc aac tct tgt ggc cag tgc ttg aag tgt ttg ggc ggt aag cct	403
Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys Leu Gly Gly Lys Pro	
90 95 100	
gcg tac tgt gag aaa ttc tat gac cgc aac ttc gca tgc acc cgc gat	451
Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe Ala Cys Thr Arg Asp	
105 110 115	
gcc ggg cac act act ttg ttt acc cgt gca aca aaa gag cag gca gag	499
Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr Lys Glu Gln Ala Glu	
120 125 130	
gcc atc atc gac acc ctt gat gat gtt ttc tac gat gcg gat gcg ggt	547
Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr Asp Ala Asp Ala Gly	
135 140 145	
ttc ctg gca tac cca gca act ccc cca gag gct tcg gga gta agc gtg	595
Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala Ser Gly Val Ser Val	
150 155 160 165	
ttg gtt gtc gcg gct ggt acc tct gat ctc ccc caa gca aag gaa gca	643
Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro Gln Ala Lys Glu Ala	
170 175 180	
cta cac act gcc tcc tac ttg ggg cgc tcc acc tca ctg att gtt gat	691
Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr Ser Leu Ile Val Asp	
185 190 195	
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Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser Tyr Glu Glu Glu Leu	
200 205 210	
cgc gct gcg ggc gtg ctc atc gtt gcc gct gga atg gat ggt gcg cta	787
Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly Met Asp Gly Ala Leu	
215 220 225	
ccc gga gtt gtc gca ggc tta gtg tcc gca cct gtc gtc gca ctg cca	835
Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro Val Val Ala Leu Pro	
230 235 240 245	
acc tcc gtg gga tac ggc gca ggt gct gga gga atc gca cca ctt ctg	883
Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly Ile Ala Pro Leu Leu	
250 255 260	
acc atg ctt aac gcc tgc gcg ccg gga gtt gga gtg gtc aac att gat	931
Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly Val Val Asn Ile Asp	
265 270 275	
aac ggc tat gga gca gga cac ctg gct gcg cag att gcg gcg agg	976
Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln Ile Ala Ala Arg	
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<213> *Corynebacterium glutamicum*

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Arg Val Ile Ala Ala Gly Val Arg His Thr Asp Ala Ile Val Arg Asp
 35 40 45

Gln Ile Tyr Pro Thr Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala
 50 55 60

Gly Val Val Val Ala Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp
 65 70 75 80

Asp Lys Val Val Leu Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys
 85 90 95

Leu Gly Gly Lys Pro Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe
 100 105 110

Ala Cys Thr Arg Asp Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr
 115 120 125

Lys Glu Gln Ala Glu Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr
 130 135 140

Asp Ala Asp Ala Gly Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala
 145 150 155 160

Ser Gly Val Ser Val Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro
 165 170 175

Gln Ala Lys Glu Ala Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr
 180 185 190

Ser Leu Ile Val Asp Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser
 195 200 205

Tyr Glu Glu Glu Leu Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly
 210 215 220

Met Asp Gly Ala Leu Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro
 225 230 235 240

Val Val Ala Leu Pro Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly
 245 250 255

Ile Ala Pro Leu Leu Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly
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Ile Ala Ala Arg
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aag	atc	gca	aac	gtc	ctg	tcg	aac	cgt	tac	gcc	tcc	gcg	gaa	ctt	tct	163
Lys	Ile	Ala	Asn	Val	Leu	Ser	Asn	Arg	Tyr	Ala	Ser	Ala	Glu	Leu	Ser	
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aac	ctg	tgg	agt	gcc	gaa	gag	aag	atc	atc	atg	gag	cgc	cag	ctc	tgg	211
Asn	Leu	Trp	Ser	Ala	Glu	Glu	Lys	Ile	Ile	Met	Glu	Arg	Gln	Leu	Trp	
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Ile	Ala	Val	Met	Lys	Ala	Gln	Lys	Asp	Leu	Gly	Val	Glu	Ile	Pro	Ala	
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gag	gca	att	gaa	tcc	tat	gaa	gca	gtg	atc	gac	cag	gtt	gat	ttg	gca	307
Glu	Ala	Ile	Glu	Ser	Tyr	Glu	Ala	Val	Ile	Asp	Gln	Val	Asp	Leu	Ala	
	55					60					65					
agc	atc	gcc	gat	cgt	gag	cgc	gtc	acc	cgc	cac	gat	gtg	aag	gcc	cgc	355
Ser	Ile	Ala	Asp	Arg	Glu	Arg	Val	Thr	Arg	His	Asp	Val	Lys	Ala	Arg	
	70				75					80					85	
atc	gaa	gaa	ttc	aat	gca	ctg	gct	ggc	cat	gag	cac	atc	cac	aag	ggc	403
Ile	Glu	Glu	Phe	Asn	Ala	Leu	Ala	Gly	His	Glu	His	Ile	His	Lys	Gly	
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atg	acc	tcc	cgc	gac	ctc	acc	gaa	aat	gtt	gaa	cag	ctg	cag	atc	cac	451
Met	Thr	Ser	Arg	Asp	Leu	Thr	Glu	Asn	Val	Glu	Gln	Leu	Gln	Ile	His	
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cgc	tcc	ctt	gag	ctg	gtc	cgc	aac	aag	ggc	att	gca	gtt	gtt	gca	gct	499
Arg	Ser		Leu	Glu	Leu	Val	Arg	Asn	Lys	Gly	Ile	Ala	Val	Val	Ala	
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atc	gga	tcc	cgc	gca	gcg	cag	tac	caa	agc	ctg	gtc	atg	gct	ggc	cgt	547
Ile	Gly	Ser	Arg	Ala	Ala	Gln	Tyr	Gln	Ser	Leu	Val	Met	Ala	Gly	Arg	
	135					140					145					
tcc	cac	aac	gtg	gca	gcg	cag	gca	act	acc	ttg	ggc	aag	cgt	ttc	gca	595
Ser	His	Asn	Val	Ala	Ala	Gln	Ala	Thr	Thr	Leu	Gly	Lys	Arg	Phe	Ala	
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acc	gca	gct	gat	gaa	atg	ctc	gtg	gca	ctt	gag	cgc	gtc	acc	gaa	ctg	643
Thr	Ala	Ala	Asp	Glu	Met	Leu	Val	Ala	Leu	Glu	Arg	Val	Thr	Glu	Leu	

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ctc	aac	cgc	tac	cca	ctt	cgc	gga	atc	aag	ggc	cca	atg	gga	acc	gcc	691
Leu	Asn	Arg	Tyr	Pro	Leu	Arg	Gly	Ile	Lys	Gly	Pro	Met	Gly	Thr	Ala	
			185					190					195			
caa	gac	atg	ctt	gac	ctc	atg	gaa	ggc	gac	gag	gct	cgt	ctc	tcc	gat	739
Gln	Asp	Met	Leu	Asp	Leu	Met	Glu	Gly	Asp	Glu	Ala	Arg	Leu	Ser	Asp	
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ctg	gaa	acc	cgc	atc	gca	gca	cac	ctc	ggc	ttt	gat	cgc	gtc	ttc	gac	787
Leu	Glu	Thr	Arg	Ile	Ala	Ala	His	Leu	Gly	Phe	Asp	Arg	Val	Phe	Asp	
	215					220					225					
tcc	gtc	ggc	cag	gtc	tac	cca	cgt	tcc	ctt	gac	ttc	gat	gca	gta	tct	835
Ser	Val	Gly	Gln	Val	Tyr	Pro	Arg	Ser	Leu	Asp	Phe	Asp	Ala	Val	Ser	
230					235					240					245	
gct	ctg	gtt	cag	ctt	ggc	tcc	ggc	cca	tca	tcg	ctg	tcc	cac	acc	att	883
Ala	Leu	Val	Gln	Leu	Gly	Ser	Gly	Pro	Ser	Ser	Leu	Ser	His	Thr	Ile	
			250					255						260		
cgt	ctc	atg	gcc	ggc	acc	gaa	act	gtt	acc	gaa	ggt	ttt	aag	gaa	ggc	931
Arg	Leu	Met	Ala	Gly	Thr	Glu	Thr	Val	Thr	Glu	Gly	Phe	Lys	Glu	Gly	
			265					270					275			
cag	gtc	ggt	tcc	tct	gca	atg	cct	cac	aag	atg	aac	gct	cgc	tcc	tgt	979
Gln	Val	Gly	Ser	Ser	Ala	Met	Pro	His	Lys	Met	Asn	Ala	Arg	Ser	Cys	
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gag	cgc	gtg	ggc	ggc	ctg	cag	gtt	att	ctt	cgc	gga	tac	ctc	acc	atg	1027
Glu	Arg	Val	Gly	Gly	Leu	Gln	Val	Ile	Leu	Arg	Gly	Tyr	Leu	Thr	Met	
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Val	Ala	Asp	Leu	Ser	Gly	Gln	Gln	Trp	Asn	Glu	Gly	Asp	Val	Phe	Cys	
310					315					320					325	
tcc	gtg	atc	cgc	cgc	gtt	gca	ctg	cca	gac	gca	ttc	ttc	gcg	att	gac	1123
Ser	Val	Ile	Arg	Arg	Val	Ala	Leu	Pro	Asp	Ala	Phe	Phe	Ala	Ile	Asp	
				330					335					340		
gga	atg	ttt	gaa	act	ttc	ctg	aca	gtc	ctg	gat	gaa	ttc	ggt	gca	ttc	1171
Gly	Met	Phe	Glu	Thr	Phe	Leu	Thr	Val	Leu	Asp	Glu	Phe	Gly	Ala	Phe	
			345					350					355			
cct	gcc	atg	atc	gag	cgc	gaa	ctt	gag	cgt	tac	ctg	cca	ttc	ctg	gca	1219
Pro	Ala	Met	Ile	Glu	Arg	Glu	Leu	Glu	Arg	Tyr	Leu	Pro	Phe	Leu	Ala	
		360					365					370				
act	acc	cgt	atc	ctc	atg	gcc	gct	gtc	cgc	gca	ggc	gtt	ggc	cgc	gaa	1267
Thr	Thr	Arg	Ile	Leu	Met	Ala	Ala	Val	Arg	Ala	Gly	Val	Gly	Arg	Glu	
		375				380					385					
acc	gca	cac	gaa	gta	atc	aag	gaa	aac	gct	gtc	gcg	gtt	gcc	ctc	aac	1315
Thr	Ala	His	Glu	Val	Ile	Lys	Glu	Asn	Ala	Val	Ala	Val	Ala	Leu	Asn	
390					395					400					405	
atg	cgc	gaa	aat	ggc	ggt	gac	cag	gac	ctt	atc	cag	cgc	ctc	gct	gct	1363
Met	Arg	Glu	Asn	Gly	Gly	Asp	Gln	Asp	Leu	Ile	Gln	Arg	Leu	Ala	Ala	
				410					415					420		

gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct 1411
 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala
 425 430 435

gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg 1459
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val
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ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac 1507
 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp
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 Tyr Arg Pro Gly Glu Ile Leu
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Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly
 35 40 45

Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp
 50 55 60

Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His
 65 70 75 80

Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu
 85 90 95

His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu
 100 105 110

Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile
 115 120 125

Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu
 130 135 140

Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu
 145 150 155 160

Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu
 165 170 175

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly
 180 185 190

Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu

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Asp	Arg	Val	Phe	Asp	Ser	Val	Gly	Gln	Val	Tyr	Pro	Arg	Ser	Leu	Asp
225					230					235					240
Phe	Asp	Ala	Val	Ser	Ala	Leu	Val	Gln	Leu	Gly	Ser	Gly	Pro	Ser	Ser
				245					250					255	
Leu	Ser	His	Thr	Ile	Arg	Leu	Met	Ala	Gly	Thr	Glu	Thr	Val	Thr	Glu
			260					265					270		
Gly	Phe	Lys	Glu	Gly	Gln	Val	Gly	Ser	Ser	Ala	Met	Pro	His	Lys	Met
		275					280					285			
Asn	Ala	Arg	Ser	Cys	Glu	Arg	Val	Gly	Gly	Leu	Gln	Val	Ile	Leu	Arg
	290					295					300				
Gly	Tyr	Leu	Thr	Met	Val	Ala	Asp	Leu	Ser	Gly	Gln	Gln	Trp	Asn	Glu
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Gly	Asp	Val	Phe	Cys	Ser	Val	Ile	Arg	Arg	Val	Ala	Leu	Pro	Asp	Ala
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Phe	Phe	Ala	Ile	Asp	Gly	Met	Phe	Glu	Thr	Phe	Leu	Thr	Val	Leu	Asp
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Glu	Phe	Gly	Ala	Phe	Pro	Ala	Met	Ile	Glu	Arg	Glu	Leu	Glu	Arg	Tyr
		355					360					365			
Leu	Pro	Phe	Leu	Ala	Thr	Thr	Arg	Ile	Leu	Met	Ala	Ala	Val	Arg	Ala
	370						375				380				
Gly	Val	Gly	Arg	Glu	Thr	Ala	His	Glu	Val	Ile	Lys	Glu	Asn	Ala	Val
385					390					395					400
Ala	Val	Ala	Leu	Asn	Met	Arg	Glu	Asn	Gly	Gly	Asp	Gln	Asp	Leu	Ile
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Gln	Arg	Leu	Ala	Ala	Asp	Glu	Arg	Leu	Pro	Met	Ser	Glu	Ala	Asp	Leu
		420					425					430			
Glu	Ala	Ala	Leu	Ala	Asp	Arg	His	Ala	Phe	Ile	Gly	Ala	Ala	Glu	Ser
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Gln	Val	Ser	Arg	Val	Leu	Asp	Arg	Ile	Gln	Val	Leu	Val	Asp	Ala	His
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               1 5

aag gca att aaa cgc gca cta att agc gtg tat gac aag act ggc ctg 163
Lys Ala Ile Lys Arg Ala Leu Ile Ser Val Tyr Asp Lys Thr Gly Leu
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gag gat cta gcc cag gca ctt cac cgc gag aac gtg gaa att gtt tcc 211
Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn Val Glu Ile Val Ser
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acc gga tcc act gcg gcg aag att gct gag ctt ggt att cct gtt acc 259
Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu Gly Ile Pro Val Thr
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ccg gtt gag gag ctc acc ggt ttc cct gag tgc ctt gag ggc cgt gtg 307
Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys Leu Glu Gly Arg Val
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aag aca ctg cac cct aag gtt cac gct ggc atc ttg gcg gac acc cgc 355
Lys Thr Leu His Pro Lys Val His Ala Gly Ile Leu Ala Asp Thr Arg
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aag gaa gac cac ctg cgt cag ctc aag gaa ctt gag gtc gcc cca ttc 403
Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu Glu Val Ala Pro Phe
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cag ctt gtc gtg gtg aac ctg tac cca ttt gct gag acc gtt gcg tcc 451
Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala Glu Thr Val Ala Ser
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ggc gcc gat ttc gat gct tgc gtt gag cag atc gac atc gga ggc cca 499
Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile Asp Ile Gly Gly Pro
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tcc atg gtt cgt gct gcg gca aag aac cac cca tct gtc gct gtg gtt 547
Ser Met Val Arg Ala Ala Ala Lys Asn His Pro Ser Val Ala Val Val
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gtt tca ccg aac cgc tac gag gat gtc cag gaa gct ttg aag acc ggt 595
Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu Ala Leu Lys Thr Gly
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gga ttc tcc cgc gcg gag cgc acc aag ttg gct gct gag gct ttc cgc 643
Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala Ala Glu Ala Phe Arg
               170 175 180

cac acc gca acc tac gat gtc acc gtt gca acc tgg atg agc gag cag 691
His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr Trp Met Ser Glu Gln
               185 190 195

ctg gct gcc gaa gat tct gag act gag ttc cca ggt tgg atc ggc acc 739
Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro Gly Trp Ile Gly Thr
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acc aac acc ttg tcc cgc agc ttg cgt tac ggt gag aac cct cac cag	787
Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly Glu Asn Pro His Gln	
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tct gca gct ttg tac gtg ggc aac acc cgc gga ctt gca cag gct aag	835
Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly Leu Ala Gln Ala Lys	
230 235 240 245	
cag ttc cac ggc aag gaa atg agc tac aac aac tac acc gat tct gat	883
Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn Tyr Thr Asp Ser Asp	
250 255 260	
gct gca tgg cgt gca gcg tgg gat cac gag cgt cct tgt gta gct atc	931
Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg Pro Cys Val Ala Ile	
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atc aag cat gca aac cct tgt ggc att gct gtt tct gat gag tcc atc	979
Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val Ser Asp Glu Ser Ile	
280 285 290	
gca gcg gca cac cgc gag gca cac gca tgt gac tct gtg tcc gca ttc	1027
Ala Ala Ala His Arg Glu Ala His Ala Cys Asp Ser Val Ser Ala Phe	
295 300 305	
ggc ggc gtc atc gcg tcc aac cgt gaa gtc agc gtt gag atg gct aac	1075
Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser Val Glu Met Ala Asn	
310 315 320 325	
cag gtt gca gag atc ttc act gag gtc atc atc gct cct tcc tat gaa	1123
Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile Ala Pro Ser Tyr Glu	
330 335 340	
gag ggc gct gtg gag atc ctg agc cag aag aag aac atc cgt att ctt	1171
Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys Asn Ile Arg Ile Leu	
345 350 355	
cag gct gaa gca cct gtg cgt aag ggc ttt gag tcc cgt gag atc tcc	1219
Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu Ser Arg Glu Ile Ser	
360 365 370	
ggc ggt ctg ctt gtt cag gaa cgc gac ttg atc cac gct gag ggc gac	1267
Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile His Ala Glu Gly Asp	
375 380 385	
aac tcc gca aac tgg act ctt gct gcc ggc tct gct gtt tct cct gag	1315
Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser Ala Val Ser Pro Glu	
390 395 400 405	
gtt ctg aag gac ctg gag ttc gcg tgg act gca gtt cgt tcc gtg aag	1363
Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala Val Arg Ser Val Lys	
410 415 420	
tcc aac gca att ctg ttg gct aag aac ggc gct acc gtt ggc gtt ggc	1411
Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala Thr Val Gly Val Gly	
425 430 435	
atg gga cag gtc aac cgc gtt gac tct gct cgc ttg gct gtc gac cgt	1459
Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg Leu Ala Val Asp Arg	
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gca ggt gca gag cgc gct acc ggt tcc gtt gct gct tcc gat gcg ttc 1507
 Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala Ala Ser Asp Ala Phe
 455 460 465

ttc cca ttc gct gat ggc ttt gag gtt ctc gct gag gct ggc atc act 1555
 Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala Glu Ala Gly Ile Thr
 470 475 480 485

gct gtt gtg cag cct ggt gga tcc att cgc gac aac gag gtc att gag 1603
 Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp Asn Glu Val Ile Glu
 490 495 500

gca gcc aac aag gct ggc gtg acc atg tac ctg act ggt gcg cga cac 1651
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 35 40 45

Gly Ile Pro Val Thr Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys
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Leu Glu Gly Arg Val Lys Thr Leu His Pro Lys Val His Ala Gly Ile
 65 70 75 80

Leu Ala Asp Thr Arg Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu
 85 90 95

Glu Val Ala Pro Phe Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala
 100 105 110

Glu Thr Val Ala Ser Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile
 115 120 125

Asp Ile Gly Gly Pro Ser Met Val Arg Ala Ala Ala Lys Asn His Pro
 130 135 140

Ser Val Ala Val Val Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu
 145 150 155 160

Ala Leu Lys Thr Gly Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala
 165 170 175

Ala Glu Ala Phe Arg His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr

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Trp	Met	Ser	Glu	Gln	Leu	Ala	Ala	Glu	Asp	Ser	Glu	Thr	Glu	Phe	Pro
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Gly	Trp	Ile	Gly	Thr	Thr	Asn	Thr	Leu	Ser	Arg	Ser	Leu	Arg	Tyr	Gly
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Glu	Asn	Pro	His	Gln	Ser	Ala	Ala	Leu	Tyr	Val	Gly	Asn	Thr	Arg	Gly
225					230			235							
Leu	Ala	Gln	Ala	Lys	Gln	Phe	His	Gly	Lys	Glu	Met	Ser	Tyr	Asn	Asn
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cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163
Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly
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Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val
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Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu
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Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg
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Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn
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Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg Arg Val Ala Glu Val
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Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val Glu Lys Leu Pro Ile	
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Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile	
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 His Gln Gln Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser
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Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
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Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
 85 90 95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
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Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
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Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg
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 165 170 175
 Gly Val Thr Lys Glu Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val
 180 185 190
 Glu Lys Leu Pro Ile Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile
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 Thr Val Lys Asp Phe Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys
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 Asp Ala Ser Gly Arg Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu
 225 230 235 240
 Glu Ser Phe Gln Arg Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile
 245 250 255
 Leu Val Val Asp Ser Ala His Ala His Ser Arg Gly Val Leu Asp Met
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 Val Ser Arg Val Lys Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly
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 Ser Val Met Leu Gly Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly
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 Glu Thr Ile Thr Ile Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met
 385 390 395 400
 Gly Ser Met Gly Ala Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg
 405 410 415
 Ser Tyr Ser Lys Asp Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp
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 Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro
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 Ile Gly Asp Ile Ile His Gln Gln Val Gly Gly Leu Arg Ala Ala Met
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Gly Tyr Thr Gly Ser Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe
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Gln Gln Thr Val Glu Ala Pro Asn Tyr His
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<212> DNA

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Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly
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Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val
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 Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
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Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu																														
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Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys																														
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Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn																														
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 Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu
 100 105 110
 Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln
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Tyr His

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Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe Asp Thr Pro Ile Thr	
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Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp Asn Phe Thr Gln Val	
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Ala Arg Ile Tyr Ile Asp Lys Arg His Gly Gly Val Glu Asp Leu Val
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Asp Gln Ile Ile Ser Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala
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 Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln
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 Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile
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ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259
 Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala
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ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307
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tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att 355
 Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile
 70 75 80 85

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 Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala
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aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt 451
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His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala	
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Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys	
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Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly	
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Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
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Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
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Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
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Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly	
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Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val	
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Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn	
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cgt	gac	ctc	ttc	aaa	gac	gaa	gtc	cgt	gcc	gtt	ggc	cgt	gaa	ctt	ggc	1267	
Arg	Asp	Leu	Phe	Lys	Asp	Glu	Val	Arg	Ala	Val	Gly	Arg	Glu	Leu	Gly		
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Leu	Pro	Glu	Glu	Ile	Val	Gly	Arg	Gln	Pro	Phe	Pro	Gly	Pro	Gly	Leu		
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cgc	cac	gct	gac	ctg	atc	gcc	cgc	acc	gag	ctc	acc	gaa	gcc	gga	ctt	1411	
Arg	His	Ala	Asp	Leu	Ile	Ala	Arg	Thr	Glu	Leu	Thr	Glu	Ala	Gly	Leu		
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Asp	Gly	Val	Ile	Trp	Gln	Cys	Pro	Val	Val	Leu	Leu	Ala	Asp	Val	Arg		
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Ser	Val	Gly	Val	Gln	Gly	Asp	Gly	Arg	Thr	Tyr	Gly	His	Pro	Ile	Val		
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Leu	Arg	Pro	Val	Ser	Ser	Glu	Asp	Ala	Met	Thr	Ala	Asp	Trp	Thr	Arg		
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ctg	cca	tac	gag	gtt	ctg	gag	aag	atc	tcc	acc	cgc	atc	acc	aac	gaa	1603	
Leu	Pro	Tyr	Glu	Val	Leu	Glu	Lys	Ile	Ser	Thr	Arg	Ile	Thr	Asn	Glu		
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Val	Pro	Asp	Val	Asn	Arg	Val	Val	Leu	Asp	Val	Thr	Ser	Lys	Pro	Pro		
			505					510					515				
gga	acc	atc	gaa	tgg	gag	taggccttaa	atgagccttc	gtt								1692	
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Tyr	Ser	Glu	Val	Ile	Pro	His	Thr	Ala	Thr	Ala	Asp	Asp	Val	Arg	Ala
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 Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His
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 Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly
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 Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu
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 Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu
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 His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile
 180 185 190
 Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu
 195 200 205
 Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys
 210 215 220
 Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln
 225 230 235 240
 Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu
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 Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala
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 Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser
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 Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly
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 Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu
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 Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu
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 Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile
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 Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys
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 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val
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Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe
 385 390 395 400
 Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp
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 Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu
 435 440 445
 Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr
 450 455 460
 Gly His Pro Ile Val Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr
 465 470 475 480
 Ala Asp Trp Thr Arg Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr
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 Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile 35
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 Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala 50
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Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile	
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Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala	
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Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly	
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His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala	
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Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys	
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Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly	
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Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
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Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
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Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
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Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
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Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
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Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
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Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
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 Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu
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 Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly
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 Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg
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 Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr
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 Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu
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Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu
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 Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp
 100 105 110
 Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His
 115 120 125
 Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly
 130 135 140
 Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu
 145 150 155 160
 Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu
 165 170 175
 His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile
 180 185 190
 Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu
 195 200 205
 Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys
 210 215 220
 Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln
 225 230 235 240
 Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu
 245 250 255
 Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala
 260 265 270
 Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser
 275 280 285
 Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly
 290 295 300
 Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu
 305 310 315 320
 Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu
 325 330 335
 Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile
 340 345 350
 Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys
 355 360 365
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val
 370 375 380
 Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe
 385 390 395 400
 Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp

	405		410		415
Arg Leu Glu Thr	Leu Arg His Ala Asp	Leu Ile Ala Arg Thr	Glu Leu		
	420		425		430
Thr Glu Ala Gly	Leu Asp Gly Val	Ile Trp Gln Cys	Pro Val Val Leu		
	435		440		445
Leu Ala Asp Val	Arg Ser Val Gly	Val Gln Gly Asp	Gly Arg		
	450		455		460

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(670)
 <223> RXA02237

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 gcacttctcg agcgtttcgg cttcgaggat taattcttca gtg tcg ggc gat aac 115
 Val Ser Gly Asp Asn
 1 5
 caa cta gga cgg ctc gta att ctt gcg ggc ccc tca gcg gtc ggt aaa 163
 Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro Ser Ala Val Gly Lys
 10 15 20
 tcg act gtg gtt gat cgc ctc cgc aat gac gtt cca aac ctg tat ttc 211
 Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val Pro Asn Leu Tyr Phe
 25 30 35
 agt gtg tcg atg acc act agg gca cct cgt cct ggt gaa gtc gat gga 259
 Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro Gly Glu Val Asp Gly
 40 45 50
 cgt gac tac ttc tat gtc act gca cag gaa ttt cag gac aaa atc gac 307
 Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe Gln Asp Lys Ile Asp
 55 60 65
 tgt gga gag atg ctt gaa tgg gca gat atc cac ggc ggt ttg cag cgt 355
 Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His Gly Gly Leu Gln Arg
 70 75 80 85
 tca ggc act cca gca ggt ccc gtc aat gag gct cgc caa aat ggt cgg 403
 Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala Arg Gln Asn Gly Arg
 90 95 100
 cca gta ttg gtt gag gtt gat ctt gca gga gcc cga aac atc gct agc 451
 Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala Arg Asn Ile Ala Ser
 105 110 115
 tta att cca gat gca gaa acc atc ttc ctt gct cca cct tca tgg gaa 499
 Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala Pro Pro Ser Trp Glu
 120 125 130

gtt ttg gtt gaa cgc ctc act gga cgt ggc acc gaa agc gaa gac gtt 547
 Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr Glu Ser Glu Asp Val
 135 140 145

att gct cgc agg ctc gag acc gca cgc gaa gaa ttg gct gct cag agc 595
 Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu Leu Ala Ala Gln Ser
 150 155 160 165

gaa ttt aag cac gtc att atc aat gat gat gtg gat aca gcc gtc aag 643
 Glu Phe Lys His Val Ile Ile Asn Asp Asp Val Asp Thr Ala Val Lys
 170 175 180

gct att gag gat gtt ctc ctc ggc gct tagccaaaac atagagcggt 690
 Ala Ile Glu Asp Val Leu Leu Gly Ala
 185 190

agg 693

<210> 958

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 958

Val Ser Gly Asp Asn Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro
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Ser Ala Val Gly Lys Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val
 20 25 30

Pro Asn Leu Tyr Phe Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro
 35 40 45

Gly Glu Val Asp Gly Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe
 50 55 60

Gln Asp Lys Ile Asp Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His
 65 70 75 80

Gly Gly Leu Gln Arg Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala
 85 90 95

Arg Gln Asn Gly Arg Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala
 100 105 110

Arg Asn Ile Ala Ser Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala
 115 120 125

Pro Pro Ser Trp Glu Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr
 130 135 140

Glu Ser Glu Asp Val Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu
 145 150 155 160

Leu Ala Ala Gln Ser Glu Phe Lys His Val Ile Ile Asn Asp Asp Val
 165 170 175

Asp Thr Ala Val Lys Ala Ile Glu Asp Val Leu Leu Gly Ala
 180 185 190

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1390)
 <223> RXA01446

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 tgcatactcc aacttcatgg atcggatgtg acgtaaacca atg gct gca atc gtt 115
 Met Ala Ala Ile Val
 1 5
 att gtc ggc gct caa tgg ggc gat gaa ggc aaa ggt aag gcc acg gat 163
 Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys Gly Lys Ala Thr Asp
 10 15 20
 att ctc ggc gga ctc gtc gat tac gtg gtt aag ccc aat ggc ggt aac 211
 Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys Pro Asn Gly Gly Asn
 25 30 35
 aac gct gga cac act gtt gtg gtc ggc ggc gag aag tac gag cta aag 259
 Asn Ala Gly His Thr Val Val Val Gly Gly Glu Lys Tyr Glu Leu Lys
 40 45 50
 ctc ctt cct gcc ggc gtc ctc tcc gaa acg gcc acc cca att ttg ggc 307
 Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala Thr Pro Ile Leu Gly
 55 60 65
 aac ggc gtt gtg atc aac ctt gag gca ctg ttc gaa gaa atc gac ggc 355
 Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe Glu Glu Ile Asp Gly
 70 75 80 85
 ctt gag gct cgc ggt gcg gat gca tcc cgc ctg cgc atc tct gca aac 403
 Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu Arg Ile Ser Ala Asn
 90 95 100
 gct cac ctg gtt gct cca tac cac cag gtg atg gac cgt gtt cag gaa 451
 Ala His Leu Val Ala Pro Tyr His Gln Val Met Asp Arg Val Gln Glu
 105 110 115
 cgc ttc ctg ggc aag cgc gca atc ggc acc acc ggc cgt ggc atc ggc 499
 Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr Gly Arg Gly Ile Gly
 120 125 130
 cca acc tac gcg gac aaa gta tcc cgc gtg gga atc cgt gtt caa gac 547
 Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly Ile Arg Val Gln Asp
 135 140 145
 att ttc gac gaa tcc atc ctt cgt caa aaa gtc gaa tcc gcc ctg gat 595
 Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val Glu Ser Ala Leu Asp
 150 155 160 165
 tac aaa aac cag gtg ctg gtg aag atg tac aac cgc aag gcc atc gtc 643
 Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn Arg Lys Ala Ile Val
 170 175 180

gct gag gaa atc gtg cag tac ttc ctc tcc tac gct gat cgt ctg cgc	691
Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr Ala Asp Arg Leu Arg	
185 190 195	
ccc atg gtc atc gat gcc acc ttg gtg ctc aac gag gca ctt gat cag	739
Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn Glu Ala Leu Asp Gln	
200 205 210	
ggc aag cac gtt ctt atg gaa ggt ggc cag gca acc atg ctc gac gtg	787
Gly Lys His Val Leu Met Glu Gly Gly Gln Ala Thr Met Leu Asp Val	
215 220 225	
gac cac ggc acc tac cca ttc gtc acc tcc tcc aac cca acc gcc ggt	835
Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Pro Thr Ala Gly	
230 235 240 245	
ggc gca agt gtt ggt tca ggt atc ggc cca acc aag atc acc agc tcc	883
Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr Lys Ile Thr Ser Ser	
250 255 260	
ttg ggt atc atc aag gcc tac acc act cgt gtt ggt gcc ggc cca ttc	931
Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val Gly Ala Gly Pro Phe	
265 270 275	
cca act gag ctg ttt gat aag tgg ggc gag tac ctg cag acc gtc ggt	979
Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr Leu Gln Thr Val Gly	
280 285 290	
ggc gag gtc ggc gtg aac acc ggc cgt aag cgt cgc tgt ggc tgg tac	1027
Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg Arg Cys Gly Trp Tyr	
295 300 305	
gac tcc gtg att gct cgt tac gca tcc cgc gtc aac gga ttc acc gac	1075
Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val Asn Gly Phe Thr Asp	
310 315 320 325	
tac ttc ctg acc aag cta gac gtg ctc acc ggc atc ggt gaa atc cca	1123
Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly Ile Gly Glu Ile Pro	
330 335 340	
atc tgc gta gct tac gac gtt gat ggt gtt cgc cac gat gaa atg cca	1171
Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg His Asp Glu Met Pro	
345 350 355	
ctg acc cag tca gag ttc cac cac gca acc cca atc ttt gaa acc atg	1219
Leu Thr Gln Ser Glu Phe His His Ala Thr Pro Ile Phe Glu Thr Met	
360 365 370	
cct gca tgg gac gaa gac atc acc gac tgc aag acc ttc gag gat ctt	1267
Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys Thr Phe Glu Asp Leu	
375 380 385	
cca caa aag gcc cag gac tac gtc cga cgt ctg gaa gaa ctc tct ggt	1315
Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu Glu Glu Leu Ser Gly	
390 395 400 405	
gct cgc ttc tcc tac atc ggt gtt gga cct ggt cgc gat cag acc atc	1363
Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly Arg Asp Gln Thr Ile	
410 415 420	

gtc ctg cat gac gta cta gct gac aac tagtactgat aaacatcagt 1410
 Val Leu His Asp Val Leu Ala Asp Asn
 425 430

gag 1413

<210> 960

<211> 430

<212> PRT

<213> Corynebacterium glutamicum

<400> 960

Met Ala Ala Ile Val Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys
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Gly Lys Ala Thr Asp Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys
 20 25 30

Pro Asn Gly Gly Asn Asn Ala Gly His Thr Val Val Val Gly Gly Glu
 35 40 45

Lys Tyr Glu Leu Lys Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala
 50 55 60

Thr Pro Ile Leu Gly Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe
 65 70 75 80

Glu Glu Ile Asp Gly Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu
 85 90 95

Arg Ile Ser Ala Asn Ala His Leu Val Ala Pro Tyr His Gln Val Met
 100 105 110

Asp Arg Val Gln Glu Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr
 115 120 125

Gly Arg Gly Ile Gly Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly
 130 135 140

Ile Arg Val Gln Asp Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val
 145 150 155 160

Glu Ser Ala Leu Asp Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn
 165 170 175

Arg Lys Ala Ile Val Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr
 180 185 190

Ala Asp Arg Leu Arg Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn
 195 200 205

Glu Ala Leu Asp Gln Gly Lys His Val Leu Met Glu Gly Gly Gln Ala
 210 215 220

Thr Met Leu Asp Val Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser
 225 230 235 240

Asn Pro Thr Ala Gly Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr
 245 250 255

Lys Ile Thr Ser Ser Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val
 260 265 270
 Gly Ala Gly Pro Phe Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr
 275 280 285
 Leu Gln Thr Val Gly Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg
 290 295 300
 Arg Cys Gly Trp Tyr Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val
 305 310 315 320
 Asn Gly Phe Thr Asp Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly
 325 330 335
 Ile Gly Glu Ile Pro Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg
 340 345 350
 His Asp Glu Met Pro Leu Thr Gln Ser Glu Phe His His Ala Thr Pro
 355 360 365
 Ile Phe Glu Thr Met Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys
 370 375 380
 Thr Phe Glu Asp Leu Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu
 385 390 395 400
 Glu Glu Leu Ser Gly Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly
 405 410 415
 Arg Asp Gln Thr Ile Val Leu His Asp Val Leu Ala Asp Asn
 420 425 430

<210> 961
 <211> 1551
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1528)
 <223> RXA00619

<400> 961
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 cgactagggtt agtttcgggtt cgtggggaat aataatttgc gtg gct gat aaa aag 115
 Val Ala Asp Lys Lys
 1 5
 aag atc gca aac gtc ctg tcg aac cgt tac gcc tcc gcg gaa ctt tct 163
 Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
 10 15 20
 aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211
 Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
 25 30 35
 atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
 Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala

40						45					50					
gag	gca	att	gaa	tcc	tat	gaa	gca	gtg	atc	gac	cag	gtt	gat	ttg	gca	307
Glu	Ala	Ile	Glu	Ser	Tyr	Glu	Ala	Val	Ile	Asp	Gln	Val	Asp	Leu	Ala	
55			60			65										
agc	atc	gcc	gat	cgt	gag	cgc	gtc	acc	cgc	cac	gat	gtg	aag	gcc	cgc	355
Ser	Ile	Ala	Asp	Arg	Glu	Arg	Val	Thr	Arg	His	Asp	Val	Lys	Ala	Arg	85
70			75			80										
atc	gaa	gaa	ttc	aat	gca	ctg	gct	ggc	cat	gag	cac	atc	cac	aag	ggc	403
Ile	Glu	Glu	Phe	Asn	Ala	Leu	Ala	Gly	His	Glu	His	Ile	His	Lys	Gly	
90				95				100								
atg	acc	tcc	cgc	gac	ctc	acc	gaa	aat	gtt	gaa	cag	ctg	cag	atc	cac	451
Met	Thr	Ser	Arg	Asp	Leu	Thr	Glu	Asn	Val	Glu	Gln	Leu	Gln	Ile	His	
105			110			115										
cgc	tcc	ctt	gag	ctg	gtc	cgc	aac	aag	ggc	att	gca	gtt	gtt	gca	gct	499
Arg	Ser	Leu	Glu	Leu	Val	Arg	Asn	Lys	Gly	Ile	Ala	Val	Val	Ala	Ala	
120			125			130										
atc	gga	tcc	cgc	gca	gcg	cag	tac	caa	agc	ctg	gtc	atg	gct	ggc	cgt	547
Ile	Gly	Ser	Arg	Ala	Ala	Gln	Tyr	Gln	Ser	Leu	Val	Met	Ala	Gly	Arg	
135			140			145										
tcc	cac	aac	gtg	gca	gcg	cag	gca	act	acc	ttg	ggc	aag	cgt	ttc	gca	595
Ser	His	Asn	Val	Ala	Ala	Gln	Ala	Thr	Thr	Leu	Gly	Lys	Arg	Phe	Ala	
150			155			160			165							
acc	gca	gct	gat	gaa	atg	ctc	gtg	gca	ctt	gag	cgc	gtc	acc	gaa	ctg	643
Thr	Ala	Ala	Asp	Glu	Met	Leu	Val	Ala	Leu	Glu	Arg	Val	Thr	Glu	Leu	
170				175				180								
ctc	aac	cgc	tac	cca	ctt	cgc	gga	atc	aag	ggc	cca	atg	gga	acc	gcc	691
Leu	Asn	Arg	Tyr	Pro	Leu	Arg	Gly	Ile	Lys	Gly	Pro	Met	Gly	Thr	Ala	
185			190			195										
caa	gac	atg	ctt	gac	ctc	atg	gaa	ggc	gac	gag	gct	cgt	ctc	tcc	gat	739
Gln	Asp	Met	Leu	Asp	Leu	Met	Glu	Gly	Asp	Glu	Ala	Arg	Leu	Ser	Asp	
200			205			210										
ctg	gaa	acc	cgc	atc	gca	gca	cac	ctc	ggc	ttt	gat	cgc	gtc	ttc	gac	787
Leu	Glu	Thr	Arg	Ile	Ala	Ala	His	Leu	Gly	Phe	Asp	Arg	Val	Phe	Asp	
215			220			225										
tcc	gtc	ggc	cag	gtc	tac	cca	cgt	tcc	ctt	gac	ttc	gat	gca	gta	tct	835
Ser	Val	Gly	Gln	Val	Tyr	Pro	Arg	Ser	Leu	Asp	Phe	Asp	Ala	Val	Ser	
230			235			240			245							
gct	ctg	gtt	cag	ctt	ggc	tcc	ggc	cca	tca	tcg	ctg	tcc	cac	acc	att	883
Ala	Leu	Val	Gln	Leu	Gly	Ser	Gly	Pro	Ser	Ser	Leu	Ser	His	Thr	Ile	
250				255				260								
cgt	ctc	atg	gcc	ggc	acc	gaa	act	gtt	acc	gaa	ggt	ttt	aag	gaa	ggc	931
Arg	Leu	Met	Ala	Gly	Thr	Glu	Thr	Val	Thr	Glu	Gly	Phe	Lys	Glu	Gly	
265			270			275										
cag	gtc	ggt	tcc	tct	gca	atg	cct	cac	aag	atg	aac	gct	cgc	tcc	tgt	979
Gln	Val	Gly	Ser	Ser	Ala	Met	Pro	His	Lys	Met	Asn	Ala	Arg	Ser	Cys	
280			285			290										

gag cgc gtg ggc ggc ctg cag gtt att ctt cgc gga tac ctc acc atg 1027
 Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg Gly Tyr Leu Thr Met
 295 300 305

gtt gct gat ctt tcc ggc cag cag tgg aac gaa ggc gat gtc ttc tgc 1075
 Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu Gly Asp Val Phe Cys
 310 315 320 325

tcc gtg atc cgc cgc gtt gca ctg cca gac gca ttc ttc gcg att gac 1123
 Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala Phe Phe Ala Ile Asp
 330 335 340

gga atg ttt gaa act ttc ctg aca gtc ctg gat gaa ttc ggt gca ttc 1171
 Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp Glu Phe Gly Ala Phe
 345 350 355

cct gcc atg atc gag cgc gaa ctt gag cgt tac ctg cca ttc ctg gca 1219
 Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr Leu Pro Phe Leu Ala
 360 365 370

act acc cgt atc ctc atg gcc gct gtc cgc gca ggc gtt ggc cgc gaa 1267
 Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala Gly Val Gly Arg Glu
 375 380 385

acc gca cac gaa gta atc aag gaa aac gct gtc gcg gtt gcc ctc aac 1315
 Thr Ala His Glu Val Ile Lys Glu Asn Ala Val Ala Val Ala Leu Asn
 390 395 400 405

atg cgc gaa aat ggc ggt gac cag gac ctt atc cag cgc ctc gct gct 1363
 Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile Gln Arg Leu Ala Ala
 410 415 420

gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct 1411
 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala
 425 430 435

gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg 1459
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val
 440 445 450

ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac 1507
 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp
 455 460 465

tac cga cca ggt gag att ctt taaagggtttt taacggcggtt cac 1551
 Tyr Arg Pro Gly Glu Ile Leu
 470 475

<210> 962

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 962

Val Ala Asp Lys Lys Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala
 1 5 10 15

Ser Ala Glu Leu Ser Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met
 20 25 30

Glu	Arg	Gln	Leu	Trp	Ile	Ala	Val	Met	Lys	Ala	Gln	Lys	Asp	Leu	Gly
		35					40					45			
Val	Glu	Ile	Pro	Ala	Glu	Ala	Ile	Glu	Ser	Tyr	Glu	Ala	Val	Ile	Asp
	50					55					60				
Gln	Val	Asp	Leu	Ala	Ser	Ile	Ala	Asp	Arg	Glu	Arg	Val	Thr	Arg	His
	65				70					75					80
Asp	Val	Lys	Ala	Arg	Ile	Glu	Glu	Phe	Asn	Ala	Leu	Ala	Gly	His	Glu
				85					90					95	
His	Ile	His	Lys	Gly	Met	Thr	Ser	Arg	Asp	Leu	Thr	Glu	Asn	Val	Glu
			100					105					110		
Gln	Leu	Gln	Ile	His	Arg	Ser	Leu	Glu	Leu	Val	Arg	Asn	Lys	Gly	Ile
		115					120					125			
Ala	Val	Val	Ala	Ala	Ile	Gly	Ser	Arg	Ala	Ala	Gln	Tyr	Gln	Ser	Leu
	130					135					140				
Val	Met	Ala	Gly	Arg	Ser	His	Asn	Val	Ala	Ala	Gln	Ala	Thr	Thr	Leu
145					150				155						160
Gly	Lys	Arg	Phe	Ala	Thr	Ala	Ala	Asp	Glu	Met	Leu	Val	Ala	Leu	Glu
				165					170					175	
Arg	Val	Thr	Glu	Leu	Leu	Asn	Arg	Tyr	Pro	Leu	Arg	Gly	Ile	Lys	Gly
			180					185					190		
Pro	Met	Gly	Thr	Ala	Gln	Asp	Met	Leu	Asp	Leu	Met	Glu	Gly	Asp	Glu
		195					200					205			
Ala	Arg	Leu	Ser	Asp	Leu	Glu	Thr	Arg	Ile	Ala	Ala	His	Leu	Gly	Phe
	210					215					220				
Asp	Arg	Val	Phe	Asp	Ser	Val	Gly	Gln	Val	Tyr	Pro	Arg	Ser	Leu	Asp
225					230					235					240
Phe	Asp	Ala	Val	Ser	Ala	Leu	Val	Gln	Leu	Gly	Ser	Gly	Pro	Ser	Ser
				245					250					255	
Leu	Ser	His	Thr	Ile	Arg	Leu	Met	Ala	Gly	Thr	Glu	Thr	Val	Thr	Glu
			260					265					270		
Gly	Phe	Lys	Glu	Gly	Gln	Val	Gly	Ser	Ser	Ala	Met	Pro	His	Lys	Met
		275					280					285			
Asn	Ala	Arg	Ser	Cys	Glu	Arg	Val	Gly	Gly	Leu	Gln	Val	Ile	Leu	Arg
	290					295					300				
Gly	Tyr	Leu	Thr	Met	Val	Ala	Asp	Leu	Ser	Gly	Gln	Gln	Trp	Asn	Glu
305					310					315					320
Gly	Asp	Val	Phe	Cys	Ser	Val	Ile	Arg	Arg	Val	Ala	Leu	Pro	Asp	Ala
				325					330					335	
Phe	Phe	Ala	Ile	Asp	Gly	Met	Phe	Glu	Thr	Phe	Leu	Thr	Val	Leu	Asp
			340					345					350		

Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr
 355 360 365

Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala
 370 375 380

Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val
 385 390 395 400

Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile
 405 410 415

Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu
 420 425 430

Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser
 435 440 445

Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His
 450 455 460

Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu
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<210> 963

<211> 666

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(643)

<223> RXA00688

<400> 963

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 Met Arg Leu Val Leu
 1 5

ctc gga cct ccc ggt gct ggt aag ggc acc cag gct gca att ctc tct 163
 Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln Ala Ala Ile Leu Ser
 10 15 20

gag aag ctt ggc att cct cac att tct act ggc gat ctt ttc cgc gcc 211
 Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly Asp Leu Phe Arg Ala
 25 30 35

aac att ggc gaa ggt acc cct ctg ggt atc gag gcc aag cag tac atc 259
 Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu Ala Lys Gln Tyr Ile
 40 45 50

gac gct ggc aag ctg gtt cca acc gac gtg act gca cgt atg gtt gct 307
 Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr Ala Arg Met Val Ala
 55 60 65

tcc cgc ctt gct gag tcc gat gct gca gaa ggc ttc ctt ttg gat ggt 355
 Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly Phe Leu Leu Asp Gly
 70 75 80 85

ttc cca cgc acc gtt gag cag gct gac atc ttg gct aac ctg ctt tcc 403
 Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu Ala Asn Leu Leu Ser
 90 95 100

gaa gct ggc cag acc ctc gat ggt gtt gtt aac tac cag gtt tct gaa 451
 Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn Tyr Gln Val Ser Glu
 105 110 115

gac gtc gtc gtg gag cgc atg ctg tcc cgt ggt cgc gct gat gac aac 499
 Asp Val Val Val Glu Arg Met Leu Ser Arg Gly Arg Ala Asp Asp Asn
 120 125 130

gaa gag acc atc cgc acc cgt ctc ggt gtc tac cgc gac gag act gct 547
 Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr Arg Asp Glu Thr Ala
 135 140 145

cct ctg atc gat cac tac ggt gac aag atc atc aac att gag gct gaa 595
 Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile Asn Ile Glu Ala Glu
 150 155 160 165

ggc gaa gtc gaa gag atc aac gct cgt acc ctc aag gca ctg ggc aaa 643
 Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu Lys Ala Leu Gly Lys
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taagatttct tctctagtgc tgc 666

<210> 964

<211> 181

<212> PRT

<213> Corynebacterium glutamicum

<400> 964

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 20 25 30

Asp Leu Phe Arg Ala Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu
 35 40 45

Ala Lys Gln Tyr Ile Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr
 50 55 60

Ala Arg Met Val Ala Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly
 65 70 75 80

Phe Leu Leu Asp Gly Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu
 85 90 95

Ala Asn Leu Leu Ser Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn
 100 105 110

Tyr Gln Val Ser Glu Asp Val Val Val Glu Arg Met Leu Ser Arg Gly
 115 120 125

Arg Ala Asp Asp Asn Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr
 130 135 140

Arg Asp Glu Thr Ala Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile
145 150 155 160

Asn Ile Glu Ala Glu Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu
165 170 175

Lys Ala Leu Gly Lys
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<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(508)

<223> RXA00266

<400> 965

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agtgcgcgaa gcagaccacc attaggtaga atcacccaac atg act gaa cgt act 115
Met Thr Glu Arg Thr
1 5

ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163
Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu
10 15 20

atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211
Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp
25 30 35

ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259
Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His
40 45 50

gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307
Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala
55 60 65

cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355
Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp
70 75 80 85

cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403
Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly
90 95 100

acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451
Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His
105 110 115

ggg tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499
Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe
120 125 130

cct aac ctg taatttttac ggtagaaaa aaa 531
Pro Asn Leu

135

<210> 966
 <211> 136
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 966
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 Gly His Val Gly Glu Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys
 20 25 30
 Leu Ala Ala Leu Asp Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys
 35 40 45
 His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu
 50 55 60
 Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg
 65 70 75 80
 Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala
 85 90 95
 Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly
 100 105 110
 Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu
 115 120 125
 Ile Ser Ile Trp Phe Pro Asn Leu
 130 135

<210> 967
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXA00489

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 Met Arg Asp His Val
 1 5
 gaa atc ggt atc ggc cgt gag gca cga cgc acc tac agc ttg gac gat 163
 Glu Ile Gly Ile Gly Arg Glu Ala Arg Thr Tyr Ser Leu Asp Asp
 10 15 20
 att tct gtc gtt tct agc cgc cgc acc cgt tca tcc aaa gat gtc gac 211
 Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser Ser Lys Asp Val Asp
 25 30 35

acc act tgg cat att gac gcc tac aag ttt gat ctg ccg ttc atg aat	259
Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp Leu Pro Phe Met Asn	
40 45 50	
cac cca agt gat gca ttg gca agc cct gag ttt gtc att gaa atg ggc	307
His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe Val Ile Glu Met Gly	
55 60 65	
aag cag ggt ggc ctt ggc gtg atc aac gct gag ggt ctg tgg ggt cgc	355
Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu Gly Leu Trp Gly Arg	
70 75 80 85	
cat gct gat ctc gat gag gcg atc gca aag gtg att gct gcg tat gag	403
His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val Ile Ala Ala Tyr Glu	
90 95 100	
gaa ggc gac cag gct gca gcc act cgc act ctt cag gag ctg cac gca	451
Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu Gln Glu Leu His Ala	
105 110 115	
gcg cca ctg gat act gag ctg ctg agt gag cgc att gcg cag gtt cgt	499
Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg Ile Ala Gln Val Arg	
120 125 130	
gat tcc ggt gag atc gtt gct gtg cgc gtg tct cca caa aat gtt cgt	547
Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser Pro Gln Asn Val Arg	
135 140 145	
gag atc gca cca atc gtc atc aag gca ggt gct gat ctg ctg gtt atc	595
Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala Asp Leu Leu Val Ile	
150 155 160 165	
cag ggc acc ctg atc tct gca gag cac gtc aac acc ggt gga gag gcc	643
Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn Thr Gly Gly Glu Ala	
170 175 180	
ctg aac cta aag gaa ttc atc ggt tct ttg gat gtt cct gtc atc gct	691
Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp Val Pro Val Ile Ala	
185 190 195	
ggg ggc gtg aac gat tac acc acc gcg ttg cac atg atg cgt acc ggt	739
Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His Met Met Arg Thr Gly	
200 205 210	
gct gtg ggc atc atc gtc ggt ggc ggc gag aac acc aac agc cta gca	787
Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn Thr Asn Ser Leu Ala	
215 220 225	
ttg ggc atg gag gta tcc atg gcc act gcg att gct gat gtc gct gcg	835
Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile Ala Asp Val Ala Ala	
230 235 240 245	
gca cgt cgt gat tac ctg gat gag acc ggt gga cgt tac gtg cac atc	883
Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly Arg Tyr Val His Ile	
250 255 260	
att gca gat gga agc att gaa aac tcc ggt gat gta gtc aag gct att	931
Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp Val Val Lys Ala Ile	
265 270 275	

gcc tgt ggc gca gat gct gtg gtg ctg ggt tca ccg ttg gct cgc gct 979
 Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser Pro Leu Ala Arg Ala
 280 285 290

gaa gaa gct gct gga aag ggc tac ttc tgg cca gca gtg gca gcg cac 1027
 Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro Ala Val Ala Ala His
 295 300 305

cct cgt ttc cca cgc ggt gtg gtt act gag tcc gtg gac ttg gat gag 1075
 Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser Val Asp Leu Asp Glu
 310 315 320 325

gca gca cca agc ttg gag cag att ctg cat ggt ccg tct acg atg ccg 1123
 Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly Pro Ser Thr Met Pro
 330 335 340

tgg ggt gtg gaa aac ttc gaa ggt gga tta aag cgt gcg ctg gct aag 1171
 Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys Arg Ala Leu Ala Lys
 345 350 355

tgt ggc tac acc gat ttg aag agc ttc caa aag gta agc ctg cac gtt 1219
 Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys Val Ser Leu His Val
 360 365 370

aac taggtgtgtg tactcgcctc ttc 1245
 Asn

<210> 968
 <211> 374
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 968
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Tyr Ser Leu Asp Asp Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser
 20 25 30

Ser Lys Asp Val Asp Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp
 35 40 45

Leu Pro Phe Met Asn His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe
 50 55 60

Val Ile Glu Met Gly Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu
 65 70 75 80

Gly Leu Trp Gly Arg His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val
 85 90 95

Ile Ala Ala Tyr Glu Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu
 100 105 110

Gln Glu Leu His Ala Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg
 115 120 125

Ile Ala Gln Val Arg Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser
 130 135 140

Pro Gln Asn Val Arg Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala
 145 150 155 160
 Asp Leu Leu Val Ile Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn
 165 170 175
 Thr Gly Gly Glu Ala Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp
 180 185 190
 Val Pro Val Ile Ala Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His
 195 200 205
 Met Met Arg Thr Gly Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn
 210 215 220
 Thr Asn Ser Leu Ala Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile
 225 230 235 240
 Ala Asp Val Ala Ala Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly
 245 250 255
 Arg Tyr Val His Ile Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp
 260 265 270
 Val Val Lys Ala Ile Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser
 275 280 285
 Pro Leu Ala Arg Ala Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro
 290 295 300
 Ala Val Ala Ala His Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser
 305 310 315 320
 Val Asp Leu Asp Glu Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly
 325 330 335
 Pro Ser Thr Met Pro Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys
 340 345 350
 Arg Ala Leu Ala Lys Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys
 355 360 365
 Val Ser Leu His Val Asn
 370

<210> 969
 <211> 1545
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1531)
 <223> RXN02281

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gtg	gtg	cgc	atg	gaa	gca	aca	acg	atc	gat	gac	gca	atc	gcg	aag	ctc						163
Val	Val	Arg	Met	Glu	Ala	Thr	Thr	Ile	Asp	Asp	Ala	Ile	Ala	Lys	Leu						
				10					15					20							
att	gac	atc	tac	gac	acc	tcg	acc	aaa	ctg	gcc	aaa	gaa	acc	ctc	aac						211
Ile	Asp	Ile	Tyr	Asp	Thr	Ser	Thr	Lys	Leu	Ala	Lys	Glu	Thr	Leu	Asn						
			25					30					35								
aat	gag	gac	tac	gcc	gca	tac	gcc	gat	gtt	gtt	tac	ccc	aaa	ctc	acc						259
Asn	Glu	Asp	Tyr	Ala	Ala	Tyr	Ala	Asp	Val	Val	Tyr	Pro	Lys	Leu	Thr						
		40					45					50									
gtt	gac	gtg	ctg	gaa	tgg	aaa	ccc	atc	gac	cgc	acc	gaa	ccc	ttc	ggc						307
Val	Asp	Val	Leu	Glu	Trp	Lys	Pro	Ile	Asp	Arg	Thr	Glu	Pro	Phe	Gly						
	55					60				65											
tat	gtg	gat	cga	gcc	ggg	cga	tac	tcc	gcc	acc	ttg	tcc	aaa	cca	cgc						355
Tyr	Val	Asp	Arg	Ala	Gly	Arg	Tyr	Ser	Ala	Thr	Leu	Ser	Lys	Pro	Arg						
	70				75				80						85						
gtg	att	gag	cgt	tac	ctc	cgc	gaa	caa	ctc	gag	cgt	ctc	acc	agt	aat						403
Val	Ile	Glu	Arg	Tyr	Leu	Arg	Glu	Gln	Leu	Glu	Arg	Leu	Thr	Ser	Asn						
				90				95						100							
tat	ccc	tgc	aag	att	tac	gta	tct	gag	tca	gat	atc	cgc	atc	cca	ccg						451
Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro						
			105					110					115								
gag	tac	att	cgc	ggc	gca	cct	tcc	gct	acc	gaa	gct	cgc	cgt	gct	ggc						499
Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly						
		120					125					130									
gat	gtt	gca	gat	atc	atc	cca	cgc	ccc	acc	ctg	gat	gaa	gtc	cac	gac						547
Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp						
		135				140					145										
gca	att	atc	gac	ggc	gac	tgg	cac	gcc	ttc	aac	ggc	ccc	gaa	ctc	ccg						595
Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro						
				150		155				160					165						
ctt	ttc	cac	ttc	ggg	ccg	caa	cgc	ttc	gac	atc	gcc	tgc	gcc	cgc	atc						643
Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile	Ala	Cys	Ala	Arg	Ile						
				170				175						180							
gag	cac	tac	acc	ggc	atc	aac	gtg	gaa	cac	gtg	cag	aag	tac	att	ctg						691
Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu						
			185				190						195								
ttc	acc	aac	tac	gcc	atg	cac	acc	acc	gag	ttc	gtg	cat	ttt	gcc	atg						739
Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met						
		200					205					210									
tcc	gaa	ctc	acc	tcg	gaa	gac	tcc	cgc	tac	gtg	ggc	cta	tcc	ttg	cca						787
Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro						
	215					220					225										
aac	ggg	cag	gta	att	gac	cga	gag	acc	gcc	acc	agc	ctc	ggc	acg	gaa						835
Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr	Ser	Leu	Gly	Thr	Glu						

230	235							240							245			
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc	Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	883																
	250	255	260															
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca	Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	931																
	265	270	275															
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa	Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	979																
	280	285	290															
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc	Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	1027																
	295	300	305															
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att	Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile	1075																
	310	315	320															
ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa	Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu	1123																
	330	335	340															
atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac	Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp	1171																
	345	350	355															
aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac	Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn	1219																
	360	365	370															
tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc	Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser	1267																
	375	380	385															
acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga	Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly	1315																
	390	395	400															
tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg	Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu	1363																
	410	415	420															
cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac	Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr	1411																
	425	430	435															
ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa	Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu	1459																
	440	445	450															
tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg	Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg	1507																
	455	460	465															
acc ttg ggt gag gtg ccg ttt cgc taaagtctcg gaga	Thr Leu Gly Glu Val Pro Phe Arg	1545																
	470	475																

<210> 970

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 970

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Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala
 20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
 35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
 50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
 85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
 100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
 115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
 130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
 145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
 165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
 180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
 195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
 210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240

Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255

Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270

Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285

1000
900
800
700
600
500
400
300
200
100
0

Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
 325 330 335
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350
 Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser
 355 360 365
 Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn
 370 375 380
 Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr
 385 390 395 400
 Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu
 405 410 415
 Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln
 420 425 430
 Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala
 435 440 445
 Val Arg Ala Met Glu Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr
 450 455 460
 Arg Lys Leu Arg Arg Thr Leu Gly Glu Val Pro Phe Arg
 465 470 475

<210> 971
 <211> 1191
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1168)
 <223> FRXA02281

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 Val Gln Lys Asp Ser
 1 5
 gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
 10 15 20
 att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn

25				30				35								
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Asn	Glu	Asp	Tyr	Ala	Ala	Tyr	Ala	Asp	Val	Val	Tyr	Pro	Lys	Leu	Thr	
	40						45					50				
gtt	gac	gtg	ctg	gaa	tgg	aaa	ccc	atc	gac	cgc	acc	gaa	ccc	ttc	ggc	307
Val	Asp	Val	Leu	Glu	Trp	Lys	Pro	Ile	Asp	Arg	Thr	Glu	Pro	Phe	Gly	
	55					60					65					
tat	gtg	gat	cga	gcc	ggg	cga	tac	tcc	gcc	acc	ttg	tcc	aaa	cca	cgc	355
Tyr	Val	Asp	Arg	Ala	Gly	Arg	Tyr	Ser	Ala	Thr	Leu	Ser	Lys	Pro	Arg	
	70				75					80					85	
gtg	att	gag	cgt	tac	ctc	cgc	gaa	caa	ctc	gag	cgt	ctc	acc	agt	aat	403
Val	Ile	Glu	Arg	Tyr	Leu	Arg	Glu	Gln	Leu	Glu	Arg	Leu	Thr	Ser	Asn	
			90						95					100		
tat	ccc	tgc	aag	att	tac	gta	tct	gag	tca	gat	atc	cgc	atc	cca	ccg	451
Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro	
			105					110					115			
gag	tac	att	cgc	ggc	gca	cct	tcc	gct	acc	gaa	gct	cgc	cgt	gct	ggc	499
Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly	
		120					125					130				
gat	gtt	gca	gat	atc	atc	cca	cgc	ccc	acc	ctg	gat	gaa	gtc	cac	gac	547
Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp	
	135					140					145					
gca	att	atc	gac	ggc	gac	tgg	cac	gcc	ttc	aac	ggc	ccc	gaa	ctc	ccg	595
Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro	
	150				155					160					165	
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Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile	Ala	Cys	Ala	Arg	Ile	
				170					175					180		
gag	cac	tac	acc	ggc	atc	aac	gtg	gaa	cac	gtg	cag	aag	tac	att	ctg	691
Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu	
			185				190						195			
ttc	acc	aac	tac	gcc	atg	cac	acc	acc	gag	ttc	gtg	cat	ttt	gcc	atg	739
Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met	
		200					205					210				
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Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro	
	215					220					225					
aac	ggg	cag	gta	att	gac	cga	gag	acc	gcc	acc	agc	ctc	ggc	acg	gaa	835
Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr	Ser	Leu	Gly	Thr	Glu	
	230				235					240					245	
acc	ctt	gat	ctg	act	agc	cgt	ttc	caa	atg	cct	cgt	tac	gat	ctc	atc	883
Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro	Arg	Tyr	Asp	Leu	Ile	
				250					255					260		
acc	gaa	gcc	ggc	gac	ggc	att	acc	att	atc	aac	atc	ggc	gtg	ggc	cca	931
Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro	
			265				270						275			

tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa 979
 Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu
 280 285 290

gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc 1027
 Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg
 295 300 305

atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att 1075
 Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile
 310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa 1123
 Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
 330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc 1168
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<210> 972

<211> 356

<212> PRT

<213> Corynebacterium glutamicum

<400> 972

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Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
 35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
 50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
 85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
 100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
 115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
 130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
 145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile

165										170					175				
Ala	Cys	Ala	Arg	Ile	Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val				
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Gln	Lys	Tyr	Ile	Leu	Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe				
		195					200					205							
Val	His	Phe	Ala	Met	Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val				
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Gly	Leu	Ser	Leu	Pro	Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr				
225					230					235					240				
Ser	Leu	Gly	Thr	Glu	Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro				
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Arg	Tyr	Asp	Leu	Ile	Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn				
		260						265					270						
Ile	Gly	Val	Gly	Pro	Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala				
	275						280					285							
Val	Leu	Arg	Pro	Glu	Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met				
	290					295					300								
Asp	Ala	Arg	Met	Arg	Ile	Gly	Asp	Leu	Ile	Leu	Gly	Asn	Ala	Tyr	Gln				
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Arg	Glu	Asp	His	Ile	Leu	Asn	Thr	Arg	Ile	Pro	Leu	Gly	Asn	Pro	Ile				
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Pro	Ala	Ile	Pro	Glu	Ile	Gln	Lys	Ala	Leu	Glu	Ala	Ser	Val	Asp	Glu				
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 <222> (101)..(1279)
 <223> RXA00147

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 Val Ser Lys Asp Thr
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 acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg 163
 Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu
 10 15 20

 gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc 211

Val	Leu	Ala	Asp 25	Gly	Arg	Thr	Phe	Thr 30	Gly	Phe	Gly	Phe	Gly 35	Ala	Ile		
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Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr	Ala	Met	Thr	Gly	Tyr		
			40				45					50					
caa	gaa	acc	atg	acc	gat	cct	tcc	tat	cac	cgc	cag	att	ggt	gtg	gct	307	
Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg	Gln	Ile	Val	Val	Ala		
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acc	gca	cca	cag	atc	ggc	aac	acc	ggc	tgg	aac	gat	gag	gac	aac	gag	355	
Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn	Asp	Glu	Asp	Asn	Glu		
	70				75					80					85		
tcc	cgc	gac	ggc	aag	att	tgg	gtt	gca	ggc	ctt	ggt	atc	cgc	gac	ctc	403	
Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu	Val	Ile	Arg	Asp	Leu		
				90					95					100			
gca	gca	cgt	gtg	tcc	aac	tgg	cgc	gcc	acc	acc	tcc	ttg	cag	cag	gaa	451	
Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr	Ser	Leu	Gln	Gln	Glu		
			105					110					115				
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Met	Ala	Gly	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly	Ile	Asp	Thr	Arg	Ala		
		120					125					130					
ctg	gtt	cgc	cac	ctg	cgc	aat	gaa	ggt	tcc	att	gca	gcg	ggc	atc	ttc	547	
Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	Ala	Ala	Gly	Ile	Phe		
		135				140					145						
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Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu	Leu	Val	Glu	Ile	Val		
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aag	aat	cag	cca	gca	atg	acc	ggc	gca	aac	ctc	tcc	gtt	gag	gtc	tct	643	
Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	Ser	Val	Glu	Val	Ser		
				170				175						180			
gct	gat	gaa	acc	tac	gtc	atc	gaa	gct	gaa	ggc	gaa	gag	cgc	cac	acc	691	
Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	Glu	Glu	Arg	His	Thr		
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gtc	gtg	gcc	tac	gac	ctg	ggc	att	aag	caa	aac	acc	cca	cgt	cgt	ttc	739	
Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	Thr	Pro	Arg	Arg	Phe		
		200					205					210					
tct	gca	cgc	ggt	gtt	cgc	acc	gtc	atc	gtg	cct	gct	gaa	acc	cca	ttc	787	
Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	Ala	Glu	Thr	Pro	Phe		
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gag	gat	atc	aag	cag	tac	aac	cca	tca	ggc	gtg	ttc	atc	tcc	aac	ggc	835	
Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	Phe	Ile	Ser	Asn	Gly		
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cct	ggc	gat	cct	gca	gca	gca	gac	gtc	atg	gtt	gat	atc	gtc	cgc	gaa	883	
Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	Asp	Ile	Val	Arg	Glu		
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gtt	ctt	gaa	gcc	gac	att	cca	ttc	ttt	ggc	atc	tgc	ttc	ggc	aac	cag	931	
Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile	Cys	Phe	Gly	Asn	Gln		

265						270						275						
att	ctt	ggc	cgc	gca	ttc	ggc	atg	gag	acc	tac	aag	ctg	aag	ttc	ggc	979		
Ile	Leu	Gly	Arg	Ala	Phe	Gly	Met	Glu	Thr	Tyr	Lys	Leu	Lys	Phe	Gly			
		280					285					290						
cac	cgc	ggc	atc	aac	gtt	cca	gtg	aag	aac	cac	atc	acc	ggc	aag	atc	1027		
His	Arg	Gly	Ile	Asn	Val	Pro	Val	Lys	Asn	His	Ile	Thr	Gly	Lys	Ile			
		295				300					305							
gac	atc	acc	gcc	cag	aac	cac	ggc	ttc	gca	ctc	aag	ggt	gaa	gca	ggc	1075		
Asp	Ile	Thr	Ala	Gln	Asn	His	Gly	Phe	Ala	Leu	Lys	Gly	Glu	Ala	Gly			
310					315					320					325			
cag	gaa	ttc	gag	acc	gat	ttc	ggc	act	gca	att	gtc	acc	cac	acc	tgc	1123		
Gln	Glu	Phe	Glu	Thr	Asp	Phe	Gly	Thr	Ala	Ile	Val	Thr	His	Thr	Cys			
				330					335					340				
ctc	aac	gac	ggc	gtc	gtt	gaa	ggt	att	gcg	ctg	aag	tcc	gga	cgc	gca	1171		
Leu	Asn	Asp	Gly	Val	Val	Glu	Gly	Ile	Ala	Leu	Lys	Ser	Gly	Arg	Ala			
			345					350					355					
tac	tcc	gtt	cag	tac	cac	cca	gag	gcc	gct	gcc	ggc	cca	aat	gat	gca	1219		
Tyr	Ser	Val	Gln	Tyr	His	Pro	Glu	Ala	Ala	Ala	Gly	Pro	Asn	Asp	Ala			
		360					365					370						
agc	ccc	ctg	ttt	gac	cag	ttt	gtt	gag	ctg	atg	gat	gca	gac	gct	cag	1267		
Ser	Pro	Leu	Phe	Asp	Gln	Phe	Val	Glu	Leu	Met	Asp	Ala	Asp	Ala	Gln			
		375				380					385							
aag	aaa	ggc	gca	taaataacat	gccaaagcgt	tca										1302		
Lys	Lys	Gly	Ala															
390																		

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<212> PRT

<213> Corynebacterium glutamicum

<400> 974

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Gly	Phe	Gly	Ala	Ile	Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr
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Ala	Met	Thr	Gly	Tyr	Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg
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Gln	Ile	Val	Val	Ala	Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn
	65				70					75					80

Asp	Glu	Asp	Asn	Glu	Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu
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Val	Ile	Arg	Asp	Leu	Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr
			100					105					110		

Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly
 115 120 125
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile
 130 135 140
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu
 145 150 155 160
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu
 165 170 175
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly
 180 185 190
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn
 195 200 205
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro
 210 215 220
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val
 225 230 235 240
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val
 245 250 255
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile
 260 265 270
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr
 275 280 285
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His
 290 295 300
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu
 305 310 315 320
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile
 325 330 335
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu
 340 345 350
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala
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 Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met
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 Asp Ala Asp Ala Gln Lys Lys Gly Ala
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<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> RXA00145

<400> 975

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                                         Met Lys His Leu Leu
                                         1 5

tcc att agc gat ctt tcc aaa gat gag att gtt gga ttg ctg gat gaa 163
Ser Ile Ser Asp Leu Ser Lys Asp Glu Ile Val Gly Leu Leu Asp Glu
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gcg gat cgc ttt aag gag gtg ctc gaa gga cgt gaa gta aag aag ctg 211
Ala Asp Arg Phe Lys Glu Val Leu Glu Gly Arg Glu Val Lys Lys Leu
                        25 30 35

ccc acg ctg cgt ggt cgc acc att ttt acc ttg ttc tat gag aac tcc 259
Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu Phe Tyr Glu Asn Ser
                        40 45 50

acg cgc acc cgt tcg tcc ttt gaa acc gca gga aag tgg atg agc gcc 307
Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly Lys Trp Met Ser Ala
                        55 60 65

gat gtg att aac att tcg gcc tca tca tcc agc gtg aag aag ggc gag 355
Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Val Lys Lys Gly Glu
                        70 75 80 85

tcg ctg aaa gat acc ggc ttg act ttg tcg gca atc ggc gcg gat gcg 403
Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala Ile Gly Ala Asp Ala
                        90 95 100

atc atc atg cgc cac cca gcc tca ggc gcc gcg cag cag ctt gcg cag 451
Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala Gln Gln Leu Ala Gln
                        105 110 115

ttc gtc gca cca ggt ggc aac ggc ccc agc gtg atc aac gcg ggt gac 499
Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val Ile Asn Ala Gly Asp
                        120 125 130

ggt tcg cac cag cac ccc acc cag gcg ctt ctc gac gct tta acc atc 547
Gly Ser His Gln His Pro Thr Gln Ala Leu Leu Asp Ala Leu Thr Ile
                        135 140 145

cgg cag cgc acc ggc cgc att gag gga ctc aaa gtt gtc atc gtg ggc 595
Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys Val Val Ile Val Gly
                        150 155 160 165

gac tgt ttg cac tcc cgg gtg gtg cgc tcc aat gtg gat ctg ctg tcc 643
Asp Cys Leu His Ser Arg Val Val Arg Ser Asn Val Asp Leu Leu Ser
                        170 175 180

act ttg ggc gca gag gta gtg ctg gtt gct cct ccg aca ctg ctt cct 691
Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro Pro Thr Leu Leu Pro
                        185 190 195

att ggt gtg gag aac tgg cca gtc cga ttc tcc tac gac atg gac gca 739

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Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser Tyr Asp Met Asp Ala
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 gaa att gcc gac gcc gac gta gtg atg atg ctg cgc gtt cag caa gaa 787
 Glu Ile Ala Asp Ala Asp Val Val Met Met Leu Arg Val Gln Gln Glu
 215 220 225
 cgc atg cag ggt ggt ttc ttc ccc tca cac cgt gag tac gca acg ctg 835
 Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg Glu Tyr Ala Thr Leu
 230 235 240 245
 tac ggc atg tcc aaa gag cgc gaa gct cgc ctc aag gac tcc gcc atc 883
 Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu Lys Asp Ser Ala Ile
 250 255 260
 atc atg cac ccc ggc ccc atg ctt cgt ggc atg gaa att aac ttc cag 931
 Ile Met His Pro Gly Pro Met Leu Arg Gly Met Glu Ile Asn Phe Gln
 265 270 275
 gtg gca gac gca cca cgc acc gcg gta ctg cag cag gta agc aac ggt 979
 Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln Gln Val Ser Asn Gly
 280 285 290
 gtg cac atg cgc atg gcc att ttg ttc gcc ctg gtc gca ggc tct gac 1027
 Val His Met Arg Met Ala Ile Leu Phe Ala Leu Val Ala Gly Ser Asp
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 Ala Thr Ile
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 35 40 45
 Phe Tyr Glu Asn Ser Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly
 50 55 60
 Lys Trp Met Ser Ala Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser
 65 70 75 80
 Val Lys Lys Gly Glu Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala
 85 90 95
 Ile Gly Ala Asp Ala Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala
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 Gln Gln Leu Ala Gln Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val
 115 120 125

Ile Asn Ala Gly Asp Gly Ser His Gln His Pro Thr Gln Ala Leu Leu
 130 135 140
 Asp Ala Leu Thr Ile Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys
 145 150 155 160
 Val Val Ile Val Gly Asp Cys Leu His Ser Arg Val Val Arg Ser Asn
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 Val Asp Leu Leu Ser Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro
 180 185 190
 Pro Thr Leu Leu Pro Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser
 195 200 205
 Tyr Asp Met Asp Ala Glu Ile Ala Asp Ala Asp Val Val Met Met Leu
 210 215 220
 Arg Val Gln Gln Glu Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg
 225 230 235 240
 Glu Tyr Ala Thr Leu Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu
 245 250 255
 Lys Asp Ser Ala Ile Ile Met His Pro Gly Pro Met Leu Arg Gly Met
 260 265 270
 Glu Ile Asn Phe Gln Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln
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 Gln Val Ser Asn Gly Val His Met Arg Met Ala Ile Leu Phe Ala Leu
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 Val Val Asp Ser Asn
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 acc cag tat cca gaa acc ggc gca ctg gca ccg gct cct gca gac tca 163
 Thr Gln Tyr Pro Glu Thr Gly Ala Leu Ala Pro Ala Pro Ala Asp Ser
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 Leu Leu Ile Ser Asn Val Leu Val Tyr Gly Glu Gly Glu Pro Thr Asn

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gtg	ttt	gtt	aaa	gat	ggt	gtg	atc	gca	gct	atc	ggc	ggc	act	cat	gag	259		
Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile	Gly	Gly	Thr	His	Glu			
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gct	gac	cgc	acc	atc	gac	ggc	aat	ggg	gga	gtt	ctc	ctt	cca	ggg	ttc	307		
Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val	Leu	Leu	Pro	Gly	Phe			
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Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly	Arg	Glu	Asp	Thr	Glu			
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acc	att	gcc	act	ggt	tct	gcc	gcc	gca	gcc	aag	ggc	gga	ttc	acc	gca	403		
Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys	Gly	Gly	Phe	Thr	Ala			
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gta	ttc	acc	atg	gcg	aac	acc	act	cca	gtg	atg	gat	cag	ccg	gtt	atc	451		
Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met	Asp	Gln	Pro	Val	Ile			
			105					110					115					
gcg	gaa	tcc	gta	tgg	ttc	aag	ggc	caa	aac	att	ggc	ctg	tgc	gac	gtg	499		
Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile	Gly	Leu	Cys	Asp	Val			
		120					125					130						
cat	cca	gtt	gga	tcc	atc	acc	aag	ggt	ctt	gag	ggc	aag	gag	ctt	act	547		
His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu	Gly	Lys	Glu	Leu	Thr			
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Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys	Val	Arg	Met	Phe	Ser			
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Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val	Met	Arg	Arg	Ala	Leu			
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gaa	tac	gcc	aag	ggc	atg	gac	gtt	ttg	atc	gcc	cag	cac	gct	gag	gat	691		
Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala	Gln	His	Ala	Glu	Asp			
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cac	cgc	ctg	act	gag	ggc	gct	tca	gca	cac	gag	ggt	gaa	aac	gca	gct	739		
His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu	Gly	Glu	Asn	Ala	Ala			
		200					205					210						
cgt	ctg	ggt	ctg	cgc	ggc	tgg	cca	cgt	gtg	gct	gag	gaa	tcc	atc	gtg	787		
Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala	Glu	Glu	Ser	Ile	Val			
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Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly	Asn	Arg	Val	His	Ile			
	230				235					240					245			
tgc	cac	gcc	tcc	act	gaa	ggc	acc	gtg	gag	ttg	ctt	cgt	tgg	gct	aag	883		
Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu	Leu	Arg	Trp	Ala	Lys			
				250					255					260				
tcc	cag	ggc	att	cca	atc	acc	gcg	gaa	gtc	acc	ccg	cac	cac	ctc	acc	931		
Ser	Gln	Gly	Ile	Pro	Ile	Thr	Ala	Glu	Val	Thr	Pro	His	His	Leu	Thr			
			265					270					275					

ttg acc gat gag cgc ctg gaa acc tac gac gcg gtc aac aaa gtc aat 979
 Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala Val Asn Lys Val Asn
 280 285 290

ccg cca ctg cgc gaa agc cgc gat gcc gaa gcg ctc aag aag gcg ctt 1027
 Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala Leu Lys Lys Ala Leu
 295 300 305

ctc gac ggc acc atc gat gtt gtt gca acc gac cac gct cct cac ggt 1075
 Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp His Ala Pro His Gly
 310 315 320 325

tcc gaa gat aag tgc tgt gaa ttc gaa aac gcc aag cca ggc atg ctc 1123
 Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala Lys Pro Gly Met Leu
 330 335 340

gga ttg gaa acc tca ctg tcc atc atc gtg gac acc ttc gtt gcc acc 1171
 Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp Thr Phe Val Ala Thr
 345 350 355

gga ctt gca gac tgg cgc ttt gtt gcg cgc gtg atg agt gaa cgc cca 1219
 Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val Met Ser Glu Arg Pro
 360 365 370

gca gaa atc acc cgt cta cca ggc cag ggt cgc cca atc gca gaa ggt 1267
 Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg Pro Ile Ala Glu Gly
 375 380 385

gag cca gca aac ctc gcg att gtt gat cca gga aaa acc tgg aca gca 1315
 Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly Lys Thr Trp Thr Ala
 390 395 400 405

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 Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn Thr Pro Phe Glu Gly
 410 415 420

caa gaa ttc agt gcc aag gtc aca cac acc gtg ctt cgt ggc aag gtg 1411
 Gln Glu Phe Ser Ala Lys Val Thr His Thr Val Leu Arg Gly Lys Val
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tgc 1464

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<213> Corynebacterium glutamicum

<400> 978

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Leu	Leu	Pro	Gly	Phe	Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly
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Arg	Glu	Asp	Thr	Glu	Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys
				85					90					95	
Gly	Gly	Phe	Thr	Ala	Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met
			100					105					110		
Asp	Gln	Pro	Val	Ile	Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile
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Gly	Lys	Glu	Leu	Thr	Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys
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Val	Arg	Met	Phe	Ser	Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val
				165					170					175	
Met	Arg	Arg	Ala	Leu	Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala
			180					185					190		
Gln	His	Ala	Glu	Asp	His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu
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Asn	Arg	Val	His	Ile	Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu
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Pro	His	His	Leu	Thr	Leu	Thr	Asp	Glu	Arg	Leu	Glu	Thr	Tyr	Asp	Ala
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	290					295					300				
Leu	Lys	Lys	Ala	Leu	Leu	Asp	Gly	Thr	Ile	Asp	Val	Val	Ala	Thr	Asp
305					310					315					320
His	Ala	Pro	His	Gly	Ser	Glu	Asp	Lys	Cys	Cys	Glu	Phe	Glu	Asn	Ala
				325					330					335	
Lys	Pro	Gly	Met	Leu	Gly	Leu	Glu	Thr	Ser	Leu	Ser	Ile	Ile	Val	Asp
			340					345					350		
Thr	Phe	Val	Ala	Thr	Gly	Leu	Ala	Asp	Trp	Arg	Phe	Val	Ala	Arg	Val
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Met Ser Glu Arg Pro Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg
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Pro Ile Ala Glu Gly Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly
 385 390 395 400

Lys Thr Trp Thr Ala Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn
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Thr Pro Phe Glu Gly Gln Glu Phe Ser Ala Lys Val Thr His Thr Val
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<223> RXA02208

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atc atc gca gtg cac gat gat tcc ctc tcc cag gaa gtc ttc ggc gtc 96
 Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val
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acc ttc cca cga cca cta ggc ctc gcc gca ggt ttc gac aaa aac gca 144
 Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala
 35 40 45

tca atg gct gat gcc tgg ggt gcc gtt gga ttc gga tac gcc gaa ctt 192
 Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu
 50 55 60

ggc acc gtc acc gcc ttc cca cag cca gga aac ccc acc ccg cgc ctt 240
 Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu
 65 70 75 80

ttc cgc ctg cct gcc gac aaa gct atc ttg aac cgc atg gga ttc aac 288
 Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn
 85 90 95

aac ctg ggt gca gca gaa gtc gca aaa aac ctg cgc aac cgg aaa tcc 336
 Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser
 100 105 110

acc gat gtc atc ggc atc aac atc ggt aaa acc aaa gtg gtt ccc gct 384
 Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala
 115 120 125

gaa cac gca gta gat gac tac cgc cgt tct gca tct ttg tta ggt gat 432

Glu	His	Ala	Val	Asp	Asp	Tyr	Arg	Arg	Ser	Ala	Ser	Leu	Leu	Gly	Asp		
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Leu	Ala	Asp	Tyr	Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly		
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Leu	Arg	Asp	Leu	Gln	Ala	Val	Glu	Ser	Leu	Arg	Pro	Ile	Leu	Ala	Ala		
				165					170					175			
gtg	cag	gaa	tcc	acc	acc	gtc	cca	gtc	ttg	gtg	aaa	atc	gca	cca	gac	576	
Val	Gln	Glu	Ser	Thr	Thr	Val	Pro	Val	Leu	Val	Lys	Ile	Ala	Pro	Asp		
			180					185					190				
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Leu	Ser	Asp	Glu	Asp	Ile	Asp	Ala	Val	Ala	Asp	Leu	Ala	Val	Glu	Leu		
		195					200					205					
aaa	ctc	gcc	gga	atc	gta	gcc	acc	aat	acc	acc	att	tcc	cgc	gaa	ggc	672	
Lys	Leu	Ala	Gly	Ile	Val	Ala	Thr	Asn	Thr	Thr	Ile	Ser	Arg	Glu	Gly		
	210					215					220						
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Leu	Asn	Thr	Pro	Ser	Gly	Glu	Val	Glu	Ala	Met	Gly	Ala	Gly	Gly	Ile		
225					230					235					240		
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Ser	Gly	Ala	Pro	Val	Ala	Ala	Arg	Ser	Leu	Glu	Val	Leu	Lys	Arg	Leu		
				245					250					255			
tac	gca	cgg	gta	ggc	aaa	gag	atg	gtg	ttg	atc	tct	gtc	ggg	ggc	atc	816	
Tyr	Ala	Arg	Val	Gly	Lys	Glu	Met	Val	Leu	Ile	Ser	Val	Gly	Gly	Ile		
			260					265					270				
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Ser	Thr	Pro	Glu	Gln	Ala	Trp	Glu	Arg	Ile	Thr	Ser	Gly	Ala	Thr	Leu		
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ctg	cag	gga	tac	acc	cca	ttc	atc	tac	ggg	ggc	ccc	gat	tgg	atc	aga	912	
Leu	Gln	Gly	Tyr	Thr	Pro	Phe	Ile	Tyr	Gly	Gly	Pro	Asp	Trp	Ile	Arg		
	290					295					300						
gat	atc	cac	ctt	ggg	atc	gcc	aag	cag	ctg	aaa	gct	cac	ggg	ctg	cgc	960	
Asp	Ile	His	Leu	Gly	Ile	Ala	Lys	Gln	Leu	Lys	Ala	His	Gly	Leu	Arg		
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aac	atc	gct	gac	gct	gtg	ggc	agc	gaa	ttg	gag	tgg	aag	aac			1002	
Asn	Ile	Ala	Asp	Ala	Val	Gly	Ser	Glu	Leu	Glu	Trp	Lys	Asn				
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<212> PRT

<213> Corynebacterium glutamicum

<400> 980

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Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala	35	40	45
Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu	50	55	60
Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu	65	70	75
Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn	85	90	95
Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser	100	105	110
Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala	115	120	125
Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp	130	135	140
Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly	145	150	155
Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala	165	170	175
Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp	180	185	190
Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu	195	200	205
Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly	210	215	220
Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile	225	230	235
Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu	245	250	255
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile	260	265	270
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu	275	280	285
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg	290	295	300
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Met Ser Ser Asn Ser 5																
att aac gca gaa gcg cgc gct gag ctt gct gaa ctg atc aaa gag cta 163																
Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu Leu Ile Lys Glu Leu 20																
gct gtc gtc cac ggt gaa gtc acc ttg tct tct ggc aag aag gct gat 211																
Ala Val Val His Gly Glu Val Thr Leu Ser Ser Gly Lys Lys Ala Asp 35																
tac tac atc gat gtc cgt cgt gcc acc ttg cac gcg cgc gca tct cgc 259																
Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His Ala Arg Ala Ser Arg 50																
ctg atc ggt cag ctg ctg cgc gaa gcc acc gct gac tgg gac tat gac 307																
Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala Asp Trp Asp Tyr Asp 65																
gca gtt ggc ggc ctg acc ttg ggc gct gac ccg gtt gcc acc gcc atc 355																
Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro Val Ala Thr Ala Ile 85																
atg cac gcc gac ggc cgc gat atc aac gcg ttt gtg gtg cgc aag gag 403																
Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe Val Val Arg Lys Glu 100																
gcc aag aag cac ggc atg cag cgt cgc att gag ggc cct gac ctg acg 451																
Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu Gly Pro Asp Leu Thr 115																
ggc aag aag gtg ctc gtg gtg gaa gat acc acc acc acc gga aat tcc 499																
Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr Thr Thr Gly Asn Ser 130																
cct ctg aca gct gtt gcc gcg ttg cgt gaa gct ggc att gag gtt gtg 547																
Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala Gly Ile Glu Val Val 145																
ggc gtt gcc acc gtg gtc gat cgc gca acc ggt gca gat gag gtt atc 595																
Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly Ala Asp Glu Val Ile 165																
gca gcg gaa ggc ctt cct tac cgc agc ttg ctg gga ctt tct gat ctt 643																
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170

175

180

gga ctc aac taacaccccc ggccccacgg agt
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675

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<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 982

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Gly Lys Lys Ala Asp Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His
 35 40 45

Ala Arg Ala Ser Arg Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala
 50 55 60

Asp Trp Asp Tyr Asp Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro
 65 70 75 80

Val Ala Thr Ala Ile Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe
 85 90 95

Val Val Arg Lys Glu Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu
 100 105 110

Gly Pro Asp Leu Thr Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr
 115 120 125

Thr Thr Gly Asn Ser Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala
 130 135 140

Gly Ile Glu Val Val Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly
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Ala Asp Glu Val Ile Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu
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Gly Leu Ser Asp Leu Gly Leu Asn
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<212> DNA

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<223> RXA02235

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Met Thr Phe Gly Glu																5
aag ctt ctg aac gcc gcc tcc acc cgt ggc agg cta tgc gtg ggc att																163
Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg Leu Cys Val Gly Ile																20
gat ccc cac gaa agc ctg ctg acg tcc tgg ggg ctg ccg gta aac gta																211
Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly Leu Pro Val Asn Val																35
gac gga ctt gcg gag ttc tcc cgc gcc tgc gtg gag gct ttc gcc gac																259
Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val Glu Ala Phe Ala Asp																50
acc gtg gca ttg gtg aag cct cag gtg gcg ttc tat gag cgt ttc ggt																307
Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe Tyr Glu Arg Phe Gly																65
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Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile Gln Thr Leu Arg Glu																85
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Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp Pro Ala Ser Pro Leu																115
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Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu Gly Phe His Ser Leu																130
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Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly Arg Gly Val Phe Val																145
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Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu Leu Gln Asp Gln Gln																165
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Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile Val Asp Gln Ala Ala																180
gcg ctt aac gcg cct tat atg gcc cag ggc aag gct ggc aac att ggc																691
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Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro Arg Leu Ser Thr Leu																210
ggg ggc gcc att ttg atg ccc ggc gtc ggc gcc cag ggc ggc acg gca																787
Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala Gln Gly Gly Thr Ala																225

agc gac gtt gat gag att gcg gga gac atg gct cat ctt gca ttc cca 835
 Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala His Leu Ala Phe Pro
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 aat gtc tct aga agt att ttg gcg aca ggc cca gat atc gct gaa atg 883
 Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro Asp Ile Ala Glu Met
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 aag aat tct gtg gca aaa aat gct gca gac ttt cct ggt ttc ccc agg 931
 Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe Pro Gly Phe Pro Arg
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 tca tagtcgcgga aacggccctt aat 957
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<211> 278

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 984

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 35 40 45
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 Tyr Glu Arg Phe Gly Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile
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 Gln Thr Leu Arg Glu Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg
 85 90 95
 Gly Asp Ile Gly Ser Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp
 100 105 110
 Pro Ala Ser Pro Leu Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu
 115 120 125
 Gly Phe His Ser Leu Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly
 130 135 140
 Arg Gly Val Phe Val Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu
 145 150 155 160
 Leu Gln Asp Gln Gln Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile
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 Val Asp Gln Ala Ala Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys
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 Ala Gly Asn Ile Gly Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro

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Asp	Ile	Ala	Glu	Met	Lys	Asn	Ser	Val	Ala	Lys	Asn	Ala	Ala	Asp	Phe	
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 Val Thr Thr Ser Ser
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 Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Gly Gly
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 Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val Asp
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 Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu Gln
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 Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu Gly
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 Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His Gly
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Val	Ile	Phe	Gly	Ala	Gly	Met	Gly	Met	Pro	Tyr	Phe	Ser	Thr	Asp	Thr																								
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Lys	Met	Pro	Ile	Leu	Val	Phe	Asn	Leu	Leu	Thr	Glu	Gly	Asn	Ile	Ala																								
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85										90										95																			

Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met
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 Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu
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 Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr
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 Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys
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 Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp
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 Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys
 180 185 190
 Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser
 195 200 205
 Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr
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 Val Glu Ser

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 Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Glu
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 Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val
 25 30 35

gac aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag 202
 Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu
 40 45 50

att gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt 250
 Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu
 55 60 65

cag cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc 298
 Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu
 70 75 80

ggc aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat 346
 Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His
 85 90 95 100

ggc gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca 394
 Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala
 105 110 115

gaa cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc 442
 Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg
 120 125 130

gtt gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac 490
 Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp
 135 140 145

acc act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg 538
 Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu
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 Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn
 165 170 175 180

cca gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag 634
 Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu
 185 190 195

aag ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac 682
 Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp
 200 205 210

aac aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att 730
 Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile
 215 220 225

gct cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 775
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<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 988

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Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys

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Gly	Ala	Glu	Leu	Gln	Gln	Arg	Gly	Met	Asp	Arg	Ala	Arg	Ser	Asp	Tyr
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Leu	Gly	Gln	His	Gly	Val	Glu	Cys	Arg	Val	Gln	Thr	Ala	Ile	Asn	Met
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Ala	Gln	Val	Ala	Glu	Pro	Tyr	Leu	Pro	Leu	Arg	Ala	Glu	Arg	His	Leu
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Glu	Lys	Gly	Arg	Val	Val	Ile	Phe	Gly	Ala	Gly	Met	Gly	Met	Pro	Tyr
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Asp	Val	Leu	Leu	Met	Ala	Lys	Ala	Val	Asp	Gly	Val	Tyr	Ser	Asp	Asp
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Pro	Arg	Thr	Asn	Pro	Asp	Ala	Glu	Leu	Phe	Thr	Glu	Ile	Thr	Pro	Lys
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210						215					220				
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Val Glu Ser

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 Met Thr Val Pro Thr
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Trp	Ala	Asp	Glu	Asp	Gly	Glu	Leu	Gly	Pro	Val	Tyr	Gly	Val	Gln	Trp															
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Arg	Ser	Trp	Pro	Thr	Pro	Asp	Gly	Arg	His	Ile	Asp	Gln	Ile	Ser	Gly															
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<400> 990

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Thr Thr Lys Lys Val His Phe His Ser Val Val Gly Glu Leu Leu Trp
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Phe Leu Gln Gly Asp Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile
          65           70           75           80

Arg Ile Trp Asn Glu Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val
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Tyr Gly Val Gln Trp Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile
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Asp Gln Ile Ser Gly Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser
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Arg Arg Asn Ile Val Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met
          130          135          140

Ala Leu Pro Pro Cys His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly
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Lys Leu Ser Cys Gln Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly
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Val Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala
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Gln Gln Ala Gly Leu Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp
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Arg
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<222> (101)..(709)

<223> RXA00131

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Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu Val Ser Ala Leu Thr
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cag gtt att gat gca aaa gtc ctt gca ttc cca cgt tat gaa acc tcg 211
Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro Arg Tyr Glu Thr Ser
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Ile His Ala Gln Leu Ala Ala Glu Ala Leu His Gly Arg Met Gly Asp
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ctc acc gac agc gcc tac gcc atg gcc acg ctt ttc gcc ctc gac cgc 307
Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu Phe Ala Leu Asp Arg
55 60 65

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His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly Val Val Leu Leu Asp
70 75 80 85

cga tac gtc gcc tcc aac gcg gct tat acc gcc gcc aga ttg ctt gac 403
Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala Ala Arg Leu Leu Asp
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Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu Phe Gly Arg Leu Gly
105 110 115

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Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp Thr Pro Ala Glu Val
120 125 130

gcg caa gat agg gct aga cgt cga gaa gcg ctt gac tcc gcg cgt gcg 547
Ala Gln Asp Arg Ala Arg Arg Glu Ala Leu Asp Ser Ala Arg Ala
135 140 145

cgg gac cgc tat gaa tcg gat tcg gcg ctg cag caa cgc acc gcc gag 595
Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln Gln Arg Thr Ala Glu
150 155 160 165

cac tat cgc cgc ctc gcg gcg gac aac tgg gaa tca ccg tgg atc gtg 643
His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu Ser Pro Trp Ile Val
170 175 180

gtt gcc cct gat gaa gac ccc ggc cac gtt gcg cag aga atc gtg gaa 691
Val Ala Pro Asp Glu Asp Pro Gly His Val Ala Gln Arg Ile Val Glu
185 190 195

ttc ctg ggt act ata aac taatcccaat tagcaggaag gat 732
Phe Leu Gly Thr Ile Asn
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<210> 992

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 992

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Arg Tyr Glu Thr Ser Ile His Ala Gln Leu Ala Ala Glu Ala Leu His
 35 40 45

Gly Arg Met Gly Asp Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu
 50 55 60

Phe Ala Leu Asp Arg His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly
 65 70 75 80

Val Val Leu Leu Asp Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala
 85 90 95

Ala Arg Leu Leu Asp Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu
 100 105 110

Phe Gly Arg Leu Gly Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp
 115 120 125

Thr Pro Ala Glu Val Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu
 130 135 140

Asp Ser Ala Arg Ala Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln
 145 150 155 160

Gln Arg Thr Ala Glu His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu
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Ser Pro Trp Ile Val Val Ala Pro Asp Glu Asp Pro Gly His Val Ala
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Gln Arg Ile Val Glu Phe Leu Gly Thr Ile Asn
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<211> 531

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(508)

<223> RXA00266

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agtgcgcgaa gcagaccacc attaggtaga atcacccaac atg act gaa cgt act 115
 Met Thr Glu Arg Thr
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ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163
 Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu

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atc	atc	gca	cgt	att	gag	cgc	aag	ggc	ctg	aag	ctc	gct	gct	ctg	gat	211				
Ile	Ile	Ala	Arg	Ile	Glu	Arg	Lys	Gly	Leu	Lys	Leu	Ala	Ala	Leu	Asp					
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ctg	cgt	gtt	gca	gac	cgc	gag	acc	gct	gaa	aag	cac	tac	gaa	gag	cac	259				
Leu	Arg	Val	Ala	Asp	Arg	Glu	Thr	Ala	Glu	Lys	His	Tyr	Glu	Glu	His					
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gct	gac	aag	cca	ttc	ttc	ggg	gag	ctc	gtt	gaa	ttc	atc	acc	tct	gca	307				
Ala	Asp	Lys	Pro	Phe	Phe	Gly	Glu	Leu	Val	Glu	Phe	Ile	Thr	Ser	Ala					
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cct	ctg	atc	gca	ggc	atc	gtc	gaa	ggc	gag	cgt	gca	atc	gat	gca	tgg	355				
Pro	Leu	Ile	Ala	Gly	Ile	Val	Glu	Gly	Glu	Arg	Ala	Ile	Asp	Ala	Trp					
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cgt	cag	ctt	gct	ggg	ggc	acc	gac	cca	gtt	gct	aag	gca	acc	cca	ggc	403				
Arg	Gln	Leu	Ala	Gly	Gly	Thr	Asp	Pro	Val	Ala	Lys	Ala	Thr	Pro	Gly					
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acc	atc	cgc	ggc	gat	ttc	gca	ctg	act	gtt	gga	gag	aac	gtt	gtt	cac	451				
Thr	Ile	Arg	Gly	Asp	Phe	Ala	Leu	Thr	Val	Gly	Glu	Asn	Val	Val	His					
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ggg	tct	gat	tcc	cca	gag	tcc	gct	gag	cgc	gag	atc	tcc	atc	tgg	ttc	499				
Gly	Ser	Asp	Ser	Pro	Glu	Ser	Ala	Glu	Arg	Glu	Ile	Ser	Ile	Trp	Phe					
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Pro	Asn	Leu																		
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<212> PRT

<213> Corynebacterium glutamicum

<400> 994

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Leu	Ala	Ala	Leu	Asp	Leu	Arg	Val	Ala	Asp	Arg	Glu	Thr	Ala	Glu	Lys
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His	Tyr	Glu	Glu	His	Ala	Asp	Lys	Pro	Phe	Phe	Gly	Glu	Leu	Val	Glu
	50					55					60				

Phe	Ile	Thr	Ser	Ala	Pro	Leu	Ile	Ala	Gly	Ile	Val	Glu	Gly	Glu	Arg
	65				70					75					80

Ala	Ile	Asp	Ala	Trp	Arg	Gln	Leu	Ala	Gly	Gly	Thr	Asp	Pro	Val	Ala
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Lys	Ala	Thr	Pro	Gly	Thr	Ile	Arg	Gly	Asp	Phe	Ala	Leu	Thr	Val	Gly
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Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu
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Ile Ser Ile Trp Phe Pro Asn Leu
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<212> DNA

<213> Corynebacterium glutamicum

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<223> RXA00718

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 Val Thr Glu Ile Ser
 1 5

aac atg cct gcc ggt ggc ctc atc gta gcc atc gac ggg ccg tct ggc 163
 Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile Asp Gly Pro Ser Gly
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acc gga aaa tcc acc aca tcc cgc gcg ctc gca acc cgt ctc tcg gcc 211
 Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala Thr Arg Leu Ser Ala
 25 30 35

aag tac cta gat act ggt gcg atg tac cgc gtc gca acg ctt cat gtg 259
 Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val Ala Thr Leu His Val
 40 45 50

ctt aac cag ggg att gac cct gca gat agc gca gcc gtg atc gct gca 307
 Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala Ala Val Ile Ala Ala
 55 60 65

acc gct gta ttg ccg ttg tcg att tct gac gat ccc gcc tcc act gag 355
 Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp Pro Ala Ser Thr Glu
 70 75 80 85

gtg ttg ctc gcg ggc gtc gat gtg caa aag gac atc cgc gga cca gaa 403
 Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp Ile Arg Gly Pro Glu
 90 95 100

gtc acc caa aat gtc tcc gca gtg tcc gcg atc cct gag gtt cgt gaa 451
 Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile Pro Glu Val Arg Glu
 105 110 115

aac ttg gtg gcg ttg cag cgc gca ctc gcc gcc aaa gca cat cgc tgc 499
 Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala Lys Ala His Arg Cys
 120 125 130

gtc gtc gaa ggc aga gac atc gga acg gca gtg ctt gtc gac gcg ccc 547
 Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val Leu Val Asp Ala Pro
 135 140 145

atc aag gcg ttt ctc acc gcc tca gcg gaa gtc cgc gcc cag cga cgc 595
 ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val Arg Ala Gln Arg Arg
 150 155 160 165

ttt gac caa gac acc gca gca ggt cgc gac gta gat ttc gac gct gtg 643
 Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val Asp Phe Asp Ala Val
 170 175 180

ctg gca gat gtt gtt cgc cgc gat gaa cta gat tcc acc cgt gcc gcc 691
 Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp Ser Thr Arg Ala Ala
 185 190 195

tca ccg ctg aaa cca gca gat gat gca cac atc gtg gac acc tct gat 739
 Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile Val Asp Thr Ser Asp
 200 205 210

atg acc atg gat caa gta ctt gat cac ctc atc cac cta gtg gaa gcc 787
 Met Thr Met Asp Gln Val Leu Asp His Leu Ile His Leu Val Glu Ala
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<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 996

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Thr Arg Leu Ser Ala Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val
 35 40 45

Ala Thr Leu His Val Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala
 50 55 60

Ala Val Ile Ala Ala Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp
 65 70 75 80

Pro Ala Ser Thr Glu Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp
 85 90 95

Ile Arg Gly Pro Glu Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile
 100 105 110

Pro Glu Val Arg Glu Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala
 115 120 125

Lys Ala His Arg Cys Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val
 130 135 140

Leu Val Asp Ala Pro Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val
 145 150 155 160

Arg	Ala	Gln	Arg	Arg 165	Phe	Asp	Gln	Asp	Thr 170	Ala	Ala	Gly	Arg	Asp 175	Val
Asp	Phe	Asp	Ala 180	Val	Leu	Ala	Asp	Val 185	Val	Arg	Arg	Asp	Glu 190	Leu	Asp
Ser	Thr	Arg 195	Ala	Ala	Ser	Pro	Leu 200	Lys	Pro	Ala	Asp	Asp 205	Ala	His	Ile
Val	Asp 210	Thr	Ser	Asp	Met	Thr 215	Met	Asp	Gln	Val	Leu 220	Asp	His	Leu	Ile
His 225	Leu	Val	Glu	Ala	Ser 230	Ala	Glu	Arg	Ser	Asn 235	Gln				

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				Met	Thr	Ser	Ser	Arg								
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aaa	gtc	cgt	ccc	acc	aaa	cac	att	ttc	gtc	acc	ggg	gga	gtt	gtt	tcc	163
Lys	Val	Arg	Pro	Thr	Lys	His	Ile	Phe	Val	Thr	Gly	Gly	Val	Val	Ser	
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tca	ctc	ggc	aaa	ggc	ctg	acc	gca	gca	agc	ctt	ggg	caa	ttg	ctg	att	211
Ser	Leu	Gly	Lys	Gly	Leu	Thr	Ala	Ala	Ser	Leu	Gly	Gln	Leu	Leu	Ile	
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Ala	Arg	Gly	Leu	Ser	Val	Thr	Met	Gln	Lys	Leu	Asp	Pro	Tyr	Leu	Asn	
		40					45					50				
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Val	Asp	Pro	Gly	Thr	Met	Asn	Pro	Phe	Glu	His	Gly	Glu	Val	Phe	Val	
	55					60					65					
acc	gaa	gac	ggg	gca	gaa	aca	gac	ctg	gat	ttg	ggc	cac	tac	gag	cgt	355
Thr	Glu	Asp	Gly	Ala	Glu	Thr	Asp	Leu	Asp	Leu	Gly	His	Tyr	Glu	Arg	
70					75					80					85	
ttc	ctc	gat	cgc	aac	ctg	ggg	ctc	aac	gcc	aat	gtc	acc	acc	ggc	aag	403
Phe	Leu	Asp	Arg	Asn	Leu	Gly	Leu	Asn	Ala	Asn	Val	Thr	Thr	Gly	Lys	
				90					95					100		
gtg	tat	tcc	act	gtg	atc	gcc	aag	gag	cgc	agg	gga	gag	tac	ctg	ggg	451
Val	Tyr	Ser	Thr	Val	Ile	Ala	Lys	Glu	Arg	Arg	Gly	Glu	Tyr	Leu	Gly	
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Lys Thr Val Gln Val Ile Pro His Ile Thr Asp Glu Ile Lys Ala Arg	
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att ttg agc atg ggc gaa cca gat gct cat ggt aac gcc cca gac gtg	547
Ile Leu Ser Met Gly Glu Pro Asp Ala His Gly Asn Ala Pro Asp Val	
135 140 145	
gtg atc tct gag gtc ggt ggc acc gtc ggt gac att gaa tcc cag cca	595
Val Ile Ser Glu Val Gly Gly Thr Val Gly Asp Ile Glu Ser Gln Pro	
150 155 160 165	
ttc ctt gaa gca gct cgc cag gta cgc cat gaa att ggt cgt gaa aac	643
Phe Leu Glu Ala Ala Arg Gln Val Arg His Glu Ile Gly Arg Glu Asn	
170 175 180	
tgc ttc ttc atc cac tgt tct ttg gtg cca tac ttg gct acc tca ggt	691
Cys Phe Phe Ile His Cys Ser Leu Val Pro Tyr Leu Ala Thr Ser Gly	
185 190 195	
gag ctg aag acc aaa ccc acc cag cat tct gtc gca gag ctg cgc ggc	739
Glu Leu Lys Thr Lys Pro Thr Gln His Ser Val Ala Glu Leu Arg Gly	
200 205 210	
atc ggt att ttg ccg gat gct ctc gtg ctt cgt tgc gat cgg gag gtc	787
Ile Gly Ile Leu Pro Asp Ala Leu Val Leu Arg Cys Asp Arg Glu Val	
215 220 225	
cct caa ggt ctg aaa gat aag atc gcg atg atg tgc gat gtt gat tat	835
Pro Gln Gly Leu Lys Asp Lys Ile Ala Met Met Cys Asp Val Asp Tyr	
230 235 240 245	
gaa ggc gtt gta tct tgc cct gat tcc agt tct att tac aac att cca	883
Glu Gly Val Val Ser Cys Pro Asp Ser Ser Ser Ile Tyr Asn Ile Pro	
250 255 260	
gat gtc ctc tac cgc gag cac ctg gac acc ttc att att cgt cgc ctg	931
Asp Val Leu Tyr Arg Glu His Leu Asp Thr Phe Ile Ile Arg Arg Leu	
265 270 275	
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Gly Leu Pro Phe Arg Asp Val Asp Trp Ser Thr Trp His Asp Leu Leu	
280 285 290	
gaa cgg gtg aac aac cca cgc cat gag ctc acc gtc ggc atc gtg ggc	1027
Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr Val Gly Ile Val Gly	
295 300 305	
aag tac att gat ctt ccc gat gct tat ctc tca gtg gtg gaa gct gtt	1075
Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser Val Val Glu Ala Val	
310 315 320 325	
cgc gct gca ggc tac gcc aat tgg acg cgc acc aat atc aag tgg att	1123
Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr Asn Ile Lys Trp Ile	
330 335 340	
acc tca gat gat tgc gaa acc cca tct ggc gcc atg aaa gcg ctc agc	1171
Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala Met Lys Ala Leu Ser	
345 350 355	
ggc ttg gat gcc atc gtg gtt ccc gga ggt ttc ggt atc cga ggt atc	1219

Gly	Leu	Asp	Ala	Ile	Val	Val	Pro	Gly	Gly	Phe	Gly	Ile	Arg	Gly	Ile		
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Glu	Gly	Lys	Ile	Gly	Ala	Ile	Thr	Phe	Ala	Arg	Glu	His	Lys	Ile	Pro		
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ctt	ctt	ggc	cta	tgc	ctt	ggc	ctg	cag	tgc	acc	gtc	atc	gag	gca	gca	1315	
Leu	Leu	Gly	Leu	Cys	Leu	Gly	Leu	Gln	Cys	Thr	Val	Ile	Glu	Ala	Ala		
390					395					400					405		
cgc	cag	gca	gga	ctg	gag	cag	gca	tca	tcc	act	gag	ttt	gac	cca	gct	1363	
Arg	Gln	Ala	Gly	Leu	Glu	Gln	Ala	Ser	Ser	Thr	Glu	Phe	Asp	Pro	Ala		
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gca	acg	cag	cca	gtg	atc	gcc	acc	atg	gaa	gag	cag	aaa	gct	gct	gtg	1411	
Ala	Thr	Gln	Pro	Val	Ile	Ala	Thr	Met	Glu	Glu	Gln	Lys	Ala	Ala	Val		
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Ser	Gly	Glu	Ala	Asp	Leu	Gly	Gly	Thr	Met	Arg	Leu	Gly	Ala	Tyr	Pro		
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	455					460					465						
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Glu	Val	Ser	Glu	Arg	His	Arg	His	Arg	Tyr	Glu	Val	Asn	Asn	Ala	Tyr		
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cgc	gcc	cag	att	gct	gaa	ggt	tca	gat	ttg	gtc	ttc	tcc	gga	acc	tca	1603	
Arg	Ala	Gln	Ile	Ala	Glu	Gly	Ser	Asp	Leu	Val	Phe	Ser	Gly	Thr	Ser		
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Pro	Asp	Gly	His	Leu	Val	Glu	Phe	Val	Glu	Tyr	Pro	Lys	Glu	Val	His		
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cct	tat	ctg	gtg	gca	acc	cag	gcg	cac	cct	gag	tac	aaa	tct	cgt	cca	1699	
Pro	Tyr	Leu	Val	Ala	Thr	Gln	Ala	His	Pro	Glu	Tyr	Lys	Ser	Arg	Pro		
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acc	cat	gct	cat	cca	ctg	ttt	tac	ggc	ctg	gtg	aag	acc	gct	ttg	gag	1747	
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<213> Corynebacterium glutamicum

<400> 998

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 Gly Gln Leu Leu Ile Ala Arg Gly Leu Ser Val Thr Met Gln Lys Leu
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 Asp Pro Tyr Leu Asn Val Asp Pro Gly Thr Met Asn Pro Phe Glu His
 50 55 60
 Gly Glu Val Phe Val Thr Glu Asp Gly Ala Glu Thr Asp Leu Asp Leu
 65 70 75 80
 Gly His Tyr Glu Arg Phe Leu Asp Arg Asn Leu Gly Leu Asn Ala Asn
 85 90 95
 Val Thr Thr Gly Lys Val Tyr Ser Thr Val Ile Ala Lys Glu Arg Arg
 100 105 110
 Gly Glu Tyr Leu Gly Lys Thr Val Gln Val Ile Pro His Ile Thr Asp
 115 120 125
 Glu Ile Lys Ala Arg Ile Leu Ser Met Gly Glu Pro Asp Ala His Gly
 130 135 140
 Asn Ala Pro Asp Val Val Ile Ser Glu Val Gly Gly Thr Val Gly Asp
 145 150 155 160
 Ile Glu Ser Gln Pro Phe Leu Glu Ala Ala Arg Gln Val Arg His Glu
 165 170 175
 Ile Gly Arg Glu Asn Cys Phe Phe Ile His Cys Ser Leu Val Pro Tyr
 180 185 190
 Leu Ala Thr Ser Gly Glu Leu Lys Thr Lys Pro Thr Gln His Ser Val
 195 200 205
 Ala Glu Leu Arg Gly Ile Gly Ile Leu Pro Asp Ala Leu Val Leu Arg
 210 215 220
 Cys Asp Arg Glu Val Pro Gln Gly Leu Lys Asp Lys Ile Ala Met Met
 225 230 235 240
 Cys Asp Val Asp Tyr Glu Gly Val Val Ser Cys Pro Asp Ser Ser Ser
 245 250 255
 Ile Tyr Asn Ile Pro Asp Val Leu Tyr Arg Glu His Leu Asp Thr Phe
 260 265 270
 Ile Ile Arg Arg Leu Gly Leu Pro Phe Arg Asp Val Asp Trp Ser Thr
 275 280 285
 Trp His Asp Leu Leu Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr
 290 295 300
 Val Gly Ile Val Gly Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser
 305 310 315 320
 Val Val Glu Ala Val Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr
 325 330 335
 Asn Ile Lys Trp Ile Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala

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Gly	Ile	Arg	Gly	Ile	Glu	Gly	Lys	Ile	Gly	Ala	Ile	Thr	Phe	Ala	Arg
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Glu	His	Lys	Ile	Pro	Leu	Leu	Gly	Leu	Cys	Leu	Gly	Leu	Gln	Cys	Thr
385					390					395					400
Val	Ile	Glu	Ala	Ala	Arg	Gln	Ala	Gly	Leu	Glu	Gln	Ala	Ser	Ser	Thr
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Glu	Phe	Asp	Pro	Ala	Ala	Thr	Gln	Pro	Val	Ile	Ala	Thr	Met	Glu	Glu
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Gln	Lys	Ala	Ala	Val	Ser	Gly	Glu	Ala	Asp	Leu	Gly	Gly	Thr	Met	Arg
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Leu	Gly	Ala	Tyr	Pro	Ala	Thr	Leu	Glu	Glu	Gly	Ser	Leu	Val	Ala	Glu
	450					455					460				
Leu	Tyr	Gly	Thr	Thr	Glu	Val	Ser	Glu	Arg	His	Arg	His	Arg	Tyr	Glu
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Phe	Ser	Gly	Thr	Ser	Pro	Asp	Gly	His	Leu	Val	Glu	Phe	Val	Glu	Tyr
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Tyr	Lys	Ser	Arg	Pro	Thr	His	Ala	His	Pro	Leu	Phe	Tyr	Gly	Leu	Val
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 <223> RXN02234

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 Met Pro Lys Arg Ser
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 gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc 163
 Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly

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Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val	Ala	Pro	Ala	Leu	Thr	Leu				
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Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly	
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Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu	
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Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val	
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Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met	
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Glu Asp Gly Val Arg Thr Leu 520 Arg Leu Ser Leu 525 Glu Ile Arg Pro 530 Val	
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Phe Lys Thr Val Asp Thr 535 Cys Ala Ala Glu 540 Phe Glu Ala Lys Thr 545 Pro	
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Tyr Pro Val Leu Val Arg Pro 730 Ser Tyr Val Leu Gly Gly 735 Arg Gly Met 740	
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Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys															
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 Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp
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<223> FRXA02234

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acc tac gtg gag cca atc gag ccg gaa tac atc gac aag att ttc gct	96
Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala	
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aag gaa atc gag cag ggc cac cca atc gac gcc gtc ctg gca acc ctt	144
Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu	
35 40 45	
ggt ggc cag act gca ctt aac gca gct atc cag ctg gat cgc ctc ggc	192
Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly	
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atc ctg gaa aag tac ggc gtt gaa ctc atc ggt gca gac atc gat gcc	240
Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala	
65 70 75 80	
att gag cgc ggc gaa gat cgc cag aag ttc aag gat att gtc acc acc	288
Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr	
85 90 95	
atc ggt ggc gaa tcc gcg cgt tcc cgc gtc tgc cac aac atg gaa gaa	336
Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu	
100 105 110	
gtc cac gag act gtc gca gaa ctc ggc ctt cca gta gtc gtg cgt cca	384
Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro	
115 120 125	
tcc ttc act atg ggt ggc ctg ggc tcc ggt ctt gca tac aac acc gaa	432
Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu	
130 135 140	
gac ctt gag cgc atc gct ggt ggc gga ctt gct gca tct cct gaa gca	480
Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala	
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Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu	

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Glu	Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile				
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Ala	Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp				
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cag	ggg	atc	gcc	atc	atc	cgc	gag	gtc	ggc	gtg	gac	acc	ggg	gga	tgt	720			
Gln	Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys				
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aac	atc	cag	ttc	gcc	atc	aac	cca	gtt	gat	ggc	cgc	atc	atc	acc	att	768			
Asn	Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile				
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gag	atg	aac	cca	cgt	gtg	tct	cgt	tcc	tcc	gct	ctg	gca	tcc	aag	gca	816			
Glu	Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala				
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acg	ggc	ttc	cca	att	gcc	aag	atg	gct	gcc	aag	ctg	gct	atc	gga	tac	864			
Thr	Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr				
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Phe	Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala				
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Ser	Val	Gly	Glu	Val	Met	Ser	Leu	Gly	Arg	Asn	Tyr	Ile	Ala	Ala	Leu				
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Asn	Lys	Ala	Leu	Arg	Ser	Leu	Glu	Thr	Lys	Gln	Gln	Gly	Phe	Trp	Thr				
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aag	cct	gat	gag	ttc	ttc	gca	ggg	gag	cgc	gct	acc	gat	aag	gca	gct	1152			
Lys	Pro	Asp	Glu	Phe	Phe	Ala	Gly	Glu	Arg	Ala	Thr	Asp	Lys	Ala	Ala				
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gtt	ctg	gaa	gat	ctc	aag	cgc	cca	acc	gaa	ggc	cgc	ctc	tac	gac	gtt	1200			
Val	Leu	Glu	Asp	Leu	Lys	Arg	Pro	Thr	Glu	Gly	Arg	Leu	Tyr	Asp	Val				
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gag	ctg	gca	atg	cgc	ctt	ggc	gca	agc	gtg	gaa	gaa	ctc	tac	gaa	gca	1248			
Glu	Leu	Ala	Met	Arg	Leu	Gly	Ala	Ser	Val	Glu	Glu	Leu	Tyr	Glu	Ala				
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tct tct att gat cct tgg ttc ctc gcc gag ctt gaa gct ctc gtg cag	1296
Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln	
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Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu	
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cgc gaa gca aag ttc atg ggt ctg tcc gac ctg cag atc gca gcc ctt	1392
Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu	
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Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser	
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Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu	
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Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro	
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gca gct gag tct gag gtc gca cca cag act gag cgt gaa aag gtc ctg	1584
Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu	
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Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp	
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Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu	
545 550 555 560	
act gtc atg gtc aac tgc aac cca gag acc gtg tcc acc gac tac gac	1728
Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp	
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Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met	
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Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile	
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Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys	
610 615 620	
aag gct ggc gtc cct gtc att ggt acc tcc cca gag gca atc gac atg	1920
Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met	
625 630 635 640	
gct gag gac cgt ggc gag ttc ggt gca ctg ctg aac cgc gag cag ctt	1968
Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu	
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Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr	
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Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu	
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gat tac atc aac cgc gca act gag ttg tct tct gac cac cca gtg ctg	2160
Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu	
705 710 715 720	
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Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu	
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Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu	
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gaa gcc ggc att cac tcc ggt gac tcc gca tgt gca ctt cct cca atg	2304
Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met	
755 760 765	
act ttg ggc gca cag gac atc gag aag gtc cgc gaa gca acc aag aag	2352
Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys	
770 775 780	
ctg gct ctg ggc atc ggt gta cag ggc ctg atg aac gtc cag tac gca	2400
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785 790 795 800	
ctc aag gac gac atc ctc tac gtc atc gag gca aac cca cgt gca tcc	2448
Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser	
805 810 815	
cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag	2496
Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys	
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gca gca tcc cgt atc gca gtg ggc gcc acc atc aag gat ctc caa gat	2544
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835 840 845	
gag ggc atg att cct acc gag tac gac ggc ggc tcc ttg cca ctg gac	2592
Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp	
850 855 860	
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Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg	
865 870 875 880	
cgc cca gat gga aag acc ctg gac acc ctg ctt tcc cca gag atg aag	2688
Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys	
885 890 895	
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Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
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 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
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 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940
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 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960
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 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
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 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990
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 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
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 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val
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 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
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 Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
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<211> 1066

<212> PRT

<213> Corynebacterium glutamicum

<400> 1002

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 35 40 45

Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
 50 55 60
 Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
 65 70 75 80
 Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr
 85 90 95
 Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu
 100 105 110
 Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro
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 Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu
 130 135 140
 Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala
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 Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu
 165 170 175
 Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile
 180 185 190
 Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val
 195 200 205
 Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp
 210 215 220
 Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys
 225 230 235 240
 Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile
 245 250 255
 Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala
 260 265 270
 Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr
 275 280 285
 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala
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 305 310 315 320
 Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys
 325 330 335
 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu
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 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr
 355 360 365
 Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala

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Glu	Leu	Ala	Met	Arg	Leu	Gly	Ala	Ser	Val	Glu	Glu	Leu	Tyr	Glu	Ala
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Ser	Ser	Ile	Asp	Pro	Trp	Phe	Leu	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gln
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Phe	Arg	Gln	Lys	Leu	Val	Asp	Ala	Pro	Phe	Leu	Asn	Glu	Asp	Leu	Leu
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Leu	Gly	Ile	Arg	Pro	Val	Phe	Lys	Thr	Val	Asp	Thr	Cys	Ala	Ala	Glu
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Phe	Glu	Ala	Lys	Thr	Pro	Tyr	His	Tyr	Ser	Ala	Tyr	Glu	Leu	Asp	Pro
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Ile	Leu	Gly	Ser	Gly	Pro	Asn	Arg	Ile	Gly	Gln	Gly	Ile	Glu	Phe	Asp
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Tyr	Ser	Cys	Val	His	Ala	Ala	Leu	Glu	Leu	Ser	Arg	Val	Gly	Tyr	Glu
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Glu	Val	Tyr	His	Ala	Glu	Ala	Gln	Ser	Gly	Thr	Val	Ala	Gly	Val	Ile
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Ala	Glu	Asp	Arg	Gly	Glu	Phe	Gly	Ala	Leu	Leu	Asn	Arg	Glu	Gln	Leu
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Pro	Ala	Pro	Ala	Phe	Gly	Thr	Ala	Thr	Ser	Phe	Glu	Glu	Ala	Arg	Thr
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		675					680					685			
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Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu
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 Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu
 725 730 735
 Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu
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 Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met
 755 760 765
 Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys
 770 775 780
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 785 790 795 800
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 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
 820 825 830
 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp
 835 840 845
 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp
 850 855 860
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg
 865 870 875 880
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
 885 890 895
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
 900 905 910
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
 915 920 925
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
 965 970 975
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val
 1010 1015 1020

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
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Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
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Leu Gln Glu Leu Asp His Ala Val Lys Ala
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<211> 424

<212> DNA

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<222> (101)..(424)

<223> RXN00450

<400> 1003

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 Val Gly Val Leu Pro
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
 10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
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att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
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gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
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 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
 90 95 100

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 Gly Ala Arg Ile Gly Arg Ile
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<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1004

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 20 25 30
 Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
 35 40 45
 Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
 50 55 60
 Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
 65 70 75 80
 Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
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 Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
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<210> 1005

<211> 418

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(418)

<223> FRXA00450

<400> 1005

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 Val Gly Val Leu Pro
 1 5
 gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
 10 15 20
 gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
 25 30 35
 att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
 40 45 50
 gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
 55 60 65
 cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
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 gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403

418

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                                         Val Arg Ile Thr Asn
                                         1           5

gcc  cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt      163
Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly
                        10                        15                        20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat      211
Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp
                        25                        30                        35

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cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag	259
His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln	
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ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc	307
Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile	
55 60 65	
cct cgc gaa aac tct tcc gcc aca ctt ttt gaa gcc atc gaa atc tgg	355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp	
70 75 80 85	
gcc gac cgc aag acc caa gcc ttc cac atc aaa gaa gac att aaa gcg	403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala	
90 95 100	
aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac gcc gtt ggt ttc	451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe	
105 110 115	
atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa	499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu	
120 125 130	
gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag	547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln	
135 140 145	
att gtc gcc ttc ccg caa aat gcc att tac gcc tac gaa ggt gcc cag	595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln	
150 155 160 165	
aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt gcc	643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly	
170 175 180	
atc cca cac ctt gaa ccc acc cga gac gat gcc gtc gag tcg gtg aaa	691
Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys	
185 190 195	
tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac	739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His	
200 205 210	
act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc	787
Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala	
215 220 225	
gca gaa gcc gca aaa cgt gac atg gcc gca caa acc gtg gtg tct cat	835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His	
230 235 240 245	
tct gtg gcg atg gcc tat tac tca cct gcc tac atg gcg cga ctt tta	883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu	
250 255 260	
ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa	931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu	
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<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 1008

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Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg
35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys
85 90 95

Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu
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 His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr
 115 120 125
 Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu
 130 135 140
 Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala
 145 150 155 160
 Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala
 165 170 175
 Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly
 180 185 190
 Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala
 195 200 205
 Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe
 210 215 220
 Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln
 225 230 235 240
 Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr
 245 250 255
 Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala
 260 265 270
 Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly
 275 280 285
 Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly
 290 295 300
 Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro
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 Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val
 325 330 335
 Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile
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 Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala
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 Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys
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 Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile
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 <223> FRXA02272

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gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163
Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly
                        10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211
Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp
                        25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259
His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln
                        40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307
Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile
                        55 60 65

cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg 355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp
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gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg 403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala
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aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc 451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe
                        105 110 115

atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa 499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu
                        120 125 130

gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag 547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln
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att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag 595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln
                        150 155 160 165

aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc 643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly
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Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys	
185 190 195	
tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac	739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His	
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act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc	787
Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala	
215 220 225	
gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat	835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His	
230 235 240 245	
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Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu	
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Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu	
265 270 275	
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Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly	
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Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe	
295 300 305	
tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat	1075
Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp	
310 315 320 325	
cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca	1123
Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr	
330 335 340	
gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc	1171
Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala	
345 350 355	
gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg	1219
Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala	
360 365 370	
aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga	1267
Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg	
375 380 385	
aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc	1315
Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser	
390 395 400 405	
agg gag ccc gaa cag gtg gac tgg aac atc taacagccca gttgggcctc	1365
Arg Glu Pro Glu Gln Val Asp Trp Asn Ile	
410 415	

ctt

1368

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<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 1010

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 20 25 30

Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg
 35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala
 50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu
 65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys
 85 90 95

Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu
 100 105 110

His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr
 115 120 125

Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu
 130 135 140

Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala
 145 150 155 160

Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala
 165 170 175

Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly
 180 185 190

Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala
 195 200 205

Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe
 210 215 220

Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln
 225 230 235 240

Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr
 245 250 255

Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala
 260 265 270

Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly

275					280					285						
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Ile	Pro	Val	Ser	Phe	Cys	Gln	Asp	Ser	Leu	Asn	Asp	Pro	Phe	Tyr	Pro	
305					310					315					320	
Met	Gly	Asp	Gly	Asp	Leu	Leu	Arg	Ile	Leu	Asp	Ser	Gly	Leu	His	Val	
325					330					335						
Ser	His	Met	Leu	Thr	Ala	Ser	His	Leu	Lys	Asn	Ala	Leu	Ser	Phe	Ile	
340					345					350						
Thr	Thr	Asn	Pro	Ala	Gly	Asn	Leu	Gly	Leu	Asp	Asn	Tyr	Asp	Ile	Ala	
355					360					365						
Glu	Asn	Ser	Pro	Ala	Asn	Leu	Leu	Val	Leu	Asp	Ala	Ser	Ser	Glu	Lys	
370					375					380						
Glu	Ala	Val	Gln	Arg	Lys	Ala	Ser	Val	Leu	Leu	Ser	Ile	His	Arg	Gly	
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405					410					415						

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 <212> DNA
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 <223> RXN03004

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 Val Leu Leu Ser Asp
 1 5
 cgt gac att cgt aaa tca att gac gca ggc gac ttg gga att gaa cct 163
 Arg Asp Ile Arg Lys Ser Ile Asp Ala Gly Asp Leu Gly Ile Glu Pro
 10 15 20
 ttc gac gct gag ctg att cag ccg tgc agt gtc gat gtc cgc atg gac 211
 Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val Asp Val Arg Met Asp
 25 30 35
 cgc tac ttc cgg gtt ttc aat aac tct aag tac acc cac att gac cct 259
 Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr Thr His Ile Asp Pro
 40 45 50
 aag ttg aat cag gat gag ctg acc agc ctt gtt gag gtt gag gac ggc 307
 Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val Glu Val Glu Asp Gly
 55 60 65
 gag ggc ttt gtg ctg cat ccg ggt gag ttt gtg ctg gcg tcc acg ctg 355

Glu Gly Phe Val Leu His Pro Gly Glu Phe Val Leu Ala Ser Thr Leu
 70 75 80 85
 gaa aag ttc act ttg cct gcg cat ctg gct ggt cgt ttg gag ggt aag 403
 Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly Arg Leu Glu Gly Lys
 90 95 100
 tcg tct ctt ggt cgt ctt ggc ttg ttg acg cac tct act gct ggt ttc 451
 Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His Ser Thr Ala Gly Phe
 105 110 115
 att gat cct ggt ttt agt ggt tac atc acg ttg gag ttg tcc aat gtg 499
 Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu Glu Leu Ser Asn Val
 120 125 130
 gct aat ctg ccg atc acg ttg tgg ccg ggt atg aag gtg ggg cag ctg 547
 Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met Lys Val Gly Gln Leu
 135 140 145
 gct ttg ttc cag atg agt tcc cct gcg gag act 580
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 <212> PRT
 <213> Corynebacterium glutamicum
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 20 25 30
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 35 40 45
 Thr His Ile Asp Pro Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val
 50 55 60
 Glu Val Glu Asp Gly Glu Gly Phe Val Leu His Pro Gly Glu Phe Val
 65 70 75 80
 Leu Ala Ser Thr Leu Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly
 85 90 95
 Arg Leu Glu Gly Lys Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His
 100 105 110
 Ser Thr Ala Gly Phe Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu
 115 120 125
 Glu Leu Ser Asn Val Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met
 130 135 140
 Lys Val Gly Gln Leu Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr
 145 150 155 160

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<220>
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 <223> RXN03137

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 Leu Glu Leu Asn Lys
 1 5
 gca gcg tac atg ttt gag tac agc ttc gat gac atc acc gtg tcc ggc 163
 Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp Ile Thr Val Ser Gly
 10 15 20
 tac gat cca cac cca ttg atc cgc ggc aag gtc gcc gta tgatcggtgc 212
 Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val Ala Val
 25 30
 gatttgggca caa 225

<210> 1014
 <211> 34
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1014
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 Ile Thr Val Ser Gly Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val
 20 25 30
 Ala Val

<210> 1015
 <211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(613)
 <223> RXN03171

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Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu

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35					40					45					
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Gly	Met	Ile	Asp	Pro	Ala	Leu	Ser	Met	Ile	Pro	Asp	Ala	Gln	Val	Gly
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Phe	Ile	Gly	Leu	Ala	Arg	Asp	Glu	Glu	Thr	His	Glu	Pro	Val	Pro	Tyr
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	115						120					125			
Asp	Pro	Met	Leu	Ala	Thr	Gly	Gly	Ser	Leu	Leu	His	Ala	Ile	Arg	Leu
	130					135					140				
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(613)
 <223> FRXA02857

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 Met Asp Ile Thr Ile
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 gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
 10 15 20
 cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
 25 30 35
 atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50
 acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
 55 60 65
 ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355

Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
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gac gca ttg gcg gaa tct 613
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<210> 1018

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1018

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
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Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
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Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
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<223> RXA02771

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 Val Ser Glu Gln Ala
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cta agc acc ttc gac agg gca cgt gag gcc ctg gac aag aaa acc cga 163
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 Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu Phe Glu Asp Leu Thr
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ccg gtg ttg ggc gat gca gaa tca ttt gtg gcc gtg gtg gac gcc atg 259
 Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala Val Val Asp Ala Met
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gct gaa gct gca gaa aaa ctg aat gca gaa atc atc ggt ggc ttg gat 307
 Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile Ile Gly Gly Leu Asp
 55 60 65

gcg cga gga ttc ctc ctc gga tct gct gtc gct tac aaa ctc ggc cta 355
 Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala Tyr Lys Leu Gly Leu
 70 75 80 85

ggt gtg ctg gct atc cgc aag aag gga aag ctc ccc cca cct gtg gtg 403
 Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu Pro Pro Pro Val Val
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acc cag gag tat gaa ctt gaa tac ggc act gca gca ctc gag ctg ccc 451
 Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala Ala Leu Glu Leu Pro
 105 110 115

agt gaa gga atc gac att gct ggt aaa aac atc gtt ttg atc gac gat 499
 Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile Val Leu Ile Asp Asp
 120 125 130

gtg ctg gca acc ggc ggc acc ttg ggc gct gca cgt aaa cta att gaa 547
 Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala Arg Lys Leu Ile Glu
 135 140 145

tcg tgt gac gga cat gtt tcc gga tat gtt ctt gcc att gag gtc cca 595

Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu Ala Ile Glu Val Pro
 150 155 160 165

ggc ctc ggc ggt agg gat aat ctt ggt gat agg ccc gtc att gtg gtc 643
 Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg Pro Val Ile Val Val
 170 175 180

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 Arg Asp Pro Gln
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Phe Glu Asp Leu Thr Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala
 35 40 45

Val Val Asp Ala Met Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile
 50 55 60

Ile Gly Gly Leu Asp Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala
 65 70 75 80

Tyr Lys Leu Gly Leu Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu
 85 90 95

Pro Pro Pro Val Val Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala
 100 105 110

Ala Leu Glu Leu Pro Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile
 115 120 125

Val Leu Ile Asp Asp Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala
 130 135 140

Arg Lys Leu Ile Glu Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu
 145 150 155 160

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Pro Val Ile Val Val Arg Asp Pro Gln
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gaa atg gcc gac cac aaa gat ctc aat gtt cca gcc aac cca tac ggc 163
Glu Met Ala Asp His Lys Asp Leu Asn Val Pro Ala Asn Pro Tyr Gly
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acc gac att gaa tca gta ttg atc agc gaa gag aag ctc aag cag cgc 211
Thr Asp Ile Glu Ser Val Leu Ile Ser Glu Glu Lys Leu Lys Gln Arg
25 30 35

atc gcc gaa atg gcc aag cgc gtc tcc gaa gag ttc aaa gac gcc gaa 259
Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu Phe Lys Asp Ala Glu
40 45 50

gaa gac ctc atc ctg gtg tgc gtg ctc aag ggc gcg ttc tac ttc ctg 307
Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly Ala Phe Tyr Phe Leu
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gca gat ttc tcc cgc atg ctc gac atc ccc acc cag tcc gag ttc atg 355
Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr Gln Ser Glu Phe Met
70 75 80 85

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Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser Ser Gly Val Val Arg
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Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly Arg Asp Val Leu Ile
105 110 115

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Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu Ser Trp Leu Met Arg
120 125 130

aac ctg aaa aac cgc aac cct aag tcc ctc aac gtg atc acc ttg ctg 547
Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn Val Ile Thr Leu Leu
135 140 145

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Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp Met Phe Asp Ile Gly
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Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr Gly Leu Asp Phe Ala
170 175 180

gaa cgc tac cgc gac ctg cca tat gtg ggc acc ctc gag cct cac gtg 691
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<213> Corynebacterium glutamicum

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Lys Leu Lys Gln Arg Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu
 35 40 45

Phe Lys Asp Ala Glu Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly
 50 55 60

Ala Phe Tyr Phe Leu Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr
 65 70 75 80

Gln Ser Glu Phe Met Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser
 85 90 95

Ser Gly Val Val Arg Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly
 100 105 110

Arg Asp Val Leu Ile Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu
 115 120 125

Ser Trp Leu Met Arg Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn
 130 135 140

Val Ile Thr Leu Leu Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp
 145 150 155 160

Met Phe Asp Ile Gly Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr
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Gly Leu Asp Phe Ala Glu Arg Tyr Arg Asp Leu Pro Tyr Val Gly Thr
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Leu Glu Pro His Val Tyr Ser Asp
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Pro Lys Ala Val Asp Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp 85 90 95		
Val Ala Asp Thr Gly Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly 100 105 110		
Asp Gln Val Val Glu Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn 115 120 125		
Ser Val Phe Lys Pro Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile 130 135 140		
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	1 5	

cca gcg ccc gag aat ctc ctg gac gcc gag aga att cag atg atc aag	163
Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg Ile Gln Met Ile Lys	
10 15 20	

aac ttc cgc aac gaa tta acg ggg ttc atg ctc aac tac caa ttt ggc	211
Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu Asn Tyr Gln Phe Gly	
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Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu Lys Thr Glu Phe Ser	
40 45 50	

cag ctg cac gaa tac gca cct atc gag cac gta tct tca cga ttg aag	307
Gln Leu His Glu Tyr Ala Pro Ile Glu His Val Ser Ser Arg Leu Lys	
55 60 65	

aca cca gaa agc atc gtc aaa aag gtc atc cga aaa gga gac gag ctc	355
Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg Lys Gly Asp Glu Leu	
70 75 80 85	

tcc ctc gca gct atc aaa gac aca gtg ttt gat atc gca ggc att cga 403
 Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp Ile Ala Gly Ile Arg
 90 95 100
 atc gtc tgc agt ttc ctc aaa gat gcc tac gca atc gcc gat atg ctg 451
 Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala Ile Ala Asp Met Leu
 105 110 115
 acc aac caa aaa gac gtc acg gtc atc gag gcc aaa gac tac atc gct 499
 Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala Lys Asp Tyr Ile Ala
 120 125 130
 aac cca aag ccg aac ggc tac aag agt ttg cac ctt atc ctc caa gtg 547
 Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His Leu Ile Leu Gln Val
 135 140 145
 cct gtc ttc ctg tct aac tcc gtg gaa aag gtc aat gtt gaa gtc cag 595
 Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val Asn Val Glu Val Gln
 150 155 160 165
 atc cgc acc att gcc atg gac ttc tgg gca agc ctc gag cac aaa atc 643
 Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser Leu Glu His Lys Ile
 170 175 180
 tac tac aaa ttt gaa caa gaa gtt cct cag tca atc ctt gat gag ctc 691
 Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu
 185 190 195
 agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740
 Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu Val Thr
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<400> 1026

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 Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu
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 Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val
 50 55 60
 Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg
 65 70 75 80
 Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp
 85 90 95
 Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala
 100 105 110

Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala
 115 120 125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His
 130 135 140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val
 145 150 155 160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser
 165 170 175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser
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Ile Leu Asp Glu Leu Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu
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Val Thr
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 Met Ser Leu Glu Arg
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aac aca caa aaa tct tcc atg ggt gtg cga agc atg tca gcc agg ctt 163
 Asn Thr Gln Lys Ser Ser Met Gly Val Arg Ser Met Ser Ala Arg Leu
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 Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
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ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 259
 Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
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gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 307
 Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
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att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 355
 Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
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Leu	Leu	His	Asp	Thr	Val	Glu	Asp	Thr	Asp	Tyr	Ser	Leu	Asp	Asp	Leu		
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Thr	Arg	Asp	Phe	Gly	Glu	Glu	Val	Ala	Arg	Leu	Val	Asp	Gly	Val	Thr		
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Lys	Leu	Asp	Lys	Val	Ala	Leu	Gly	Ala	Ala	Ala	Glu	Ala	Glu	Thr	Ile		
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cgc	aaa	atg	atc	gtc	gcc	atg	agc	cag	gac	ccc	cgc	gtg	ctg	gtg	att	595	
Arg	Lys	Met	Ile	Val	Ala	Met	Ser	Gln	Asp	Pro	Arg	Val	Leu	Val	Ile		
	150				155					160					165		
aaa	gtg	gcc	gac	cgt	ttg	cac	aat	atg	cgc	acc	atg	cgg	ttc	ctg	ccg	643	
Lys	Val	Ala	Asp	Arg	Leu	His	Asn	Met	Arg	Thr	Met	Arg	Phe	Leu	Pro		
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Pro	Glu	Lys	Gln	Ala	Lys	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Val	Ile	Ala		
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Pro	Leu	Ala	His	Arg	Leu	Gly	Met	Ala	Ser	Val	Lys	Trp	Glu	Leu	Glu		
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cgt	ctt	gtt	gcc	gac	cgc	gag	ccc	tct	aga	gac	cgg	tac	ctc	aaa	gaa	835	
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Glu	Val	Leu	Gly	Arg	Pro	Lys	His	Tyr	Trp	Ser	Ile	Tyr	Gln	Lys	Met		
			265					270					275				
atc	gtt	cgc	ggg	cgt	gat	ttt	gac	gat	att	ttt	gat	ctt	gtt	ggc	atc	979	
Ile	Val	Arg	Gly	Arg	Asp	Phe	Asp	Asp	Ile	Phe	Asp	Leu	Val	Gly	Ile		
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cgc	atc	ctg	gta	gac	aac	gtg	aac	aac	tgt	gta	cgc	cgc	cat	cgg	tgt	1027	
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	310				315					320					325		
ttc	agc	ccc	gag	ctt	cgg	tgt	cta	cca	atc	cct	gca	cac	cac	cgt	gat	1123	
Phe	Ser	Pro	Ala	Leu	Arg	Cys	Leu	Pro	Ile	Pro	Ala	His	His	Arg	Asp		

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1158

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 35 40 45

Arg Ala Asp Val Gln Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg
 50 55 60

Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His
 65 70 75 80

Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr
 85 90 95

Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr
 100 105 110

Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu
 115 120 125

Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala
 130 135 140

Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro
 145 150 155 160

Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr
 165 170 175

Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr
 180 185 190

Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val
 195 200 205

Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys
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Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp
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Met Ser Ala Arg Leu																
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Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp																
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Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln																
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Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val																
40 45 50																
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Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala																
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Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala																
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Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu																
90 95 100																
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Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
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 Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
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 Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
 135 140 145
 aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 595
 Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
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 ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 643
 Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr Leu Glu Val Ile Ala
 170 175 180
 cct ttg gca cac cgc ctg ggc atg gcc agc gtg aaa tgg gaa ttg gaa 691
 Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu
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 gat cta tcc ttt gcc att ttg tac ccc aag aag tac gaa gag atc gtg 739
 Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val
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 cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 787
 Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu
 215 220 225
 att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 835
 Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala
 230 235 240 245
 gaa gtg ctt ggt cgn ccn aag cac tct ggt ctt tct ttc aaa aga 880
 Glu Val Leu Gly Arg Pro Lys His Ser Gly Leu Ser Phe Lys Arg
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 tgatcgttcg cggtcgtgat ttt 903

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<212> PRT

<213> Corynebacterium glutamicum

<400> 1030

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 Arg Ala Asp Val Gln Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg
 35 40 45
 Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His
 50 55 60
 Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr

65 70 75 80
 Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr
 85 90 95
 Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu
 100 105 110
 Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala
 115 120 125
 Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro
 130 135 140
 Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr
 145 150 155 160
 Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr
 165 170 175
 Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val
 180 185 190
 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys
 195 200 205
 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp
 210 215 220
 Arg Tyr Leu Lys Glu Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu
 225 230 235 240
 Asn Asn Ile Ala Ala Glu Val Leu Gly Arg Pro Lys His Ser Gly Leu
 245 250 255
 Ser Phe Lys Arg
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<210> 1031

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(262)

<223> FRXA02773

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 Met Ile Val Arg Gly
 1 5

cgt gat ttt gac gat att ttt gat ctt gtt ggc atc cgc ntc ctg gna 163
 Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly Ile Arg Xaa Leu Xaa
 10 15 20

gac aac gtg aac aac tgg gta cgc cgc cnt cgg tgt cgt gca ctc c'cn 211

Asp Asn Val Asn Asn Trp Val Arg Arg Xaa Arg Cys Arg Ala Leu Pro
 25 30 35
 gtn caa tgc tct gnc tgg ncg ntt caa aga cta tat ttc agc ccc gcg 259
 Val Gln Cys Ser Xaa Trp Xaa Xaa Gln Arg Leu Tyr Phe Ser Pro Ala
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 ctt 262
 Leu

<210> 1032
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<400> 1032
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 Cys Arg Ala Leu Pro Val Gln Cys Ser Xaa Trp Xaa Xaa Gln Arg Leu
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 Tyr Phe Ser Pro Ala Leu
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 Met Asn Thr Ala Ala
 1 5
 tgg gca cac cgc cac cac gta cgc aaa ggc ggt gga att ccg tat gtc 163
 Trp Ala His Arg His His Val Arg Lys Gly Gly Gly Ile Pro Tyr Val
 10 15 20
 agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat 211
 Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp
 25 30 35
 gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta 259
 Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val
 40 45 50
 ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307

Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg
 55 60 65
 gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg 355
 Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp
 70 75 80 85
 aaa gcg cgt gcc gac gct tac ctc ctg cac ctc agc gca ggt gcc agc 403
 Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser
 90 95 100
 tta gag gct gtc tta atc tcc acc gca gat aaa ctg cat aat ctc atg 451
 Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys Leu His Asn Leu Met
 105 110 115
 tcc atc ttg gat gac ctt gaa ata cac ggt gaa gat tta tgg caa cgc 499
 Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg
 120 125 130
 ttt aac gct ggc aaa gag cag caa atc tgg tgg tat agc gag gtt tat 547
 Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr
 135 140 145
 cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg 595
 Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu
 150 155 160 165
 ggg ttg tgc gtc gaa aag ctc tta aag caa agc gcc taggcgctcg 641
 Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser Ala
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 gcggcgctcga taa 654

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 <213> Corynebacterium glutamicum

 <400> 1034
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 Ser Val Thr Asn Asp Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp
 35 40 45
 Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala
 50 55 60
 Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln
 65 70 75 80
 Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu
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 Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys
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<223> RXA01483
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				Met	Tyr	Pro	Tyr	Ser								
						1		5								
gac	gca	gac	gct	ttt	cga	cgc	cag	cct	gag	cgc	gcc	aag	tcc	agc	caa	163
Asp	Ala	Asp	Ala	Phe	Arg	Arg	Gln	Pro	Glu	Arg	Ala	Lys	Ser	Ser	Gln	
				10					15					20		
ctg	cgt	acc	agc	gcc	gta	gac	acc	cgc	agc	gcg	ttc	gcc	cgc	gac	cgg	211
Leu	Arg	Thr	Ser	Ala	Val	Asp	Thr	Arg	Ser	Ala	Phe	Ala	Arg	Asp	Arg	
			25					30					35			
gct	cgc	gtg	ctg	cat	tct	gct	gct	ctt	cga	cgc	ctc	gcg	gat	aaa	acc	259
Ala	Arg	Val	Leu	His	Ser	Ala	Ala	Leu	Arg	Arg	Leu	Ala	Asp	Lys	Thr	
		40					45					50				
caa	gtg	gtt	ggc	ccc	aat	gat	ggt	gat	act	ccg	cgc	acc	cgg	ctg	acg	307
Gln	Val	Val	Gly	Pro	Asn	Asp	Gly	Asp	Thr	Pro	Arg	Thr	Arg	Leu	Thr	
	55					60					65					
cac	tct	ttg	gaa	gta	gct	caa	att	gca	cgg	gga	atc	gga	gct	gga	ctg	355
His	Ser	Leu	Glu	Val	Ala	Gln	Ile	Ala	Arg	Gly	Ile	Gly	Ala	Gly	Leu	
70					75					80					85	
gat	ttg	gat	cct	gat	ctg	tgc	gat	ctg	gca	ggg	ctg	tgc	cat	gac	att	403
Asp	Leu	Asp	Pro	Asp	Leu	Cys	Asp	Leu	Ala	Gly	Leu	Cys	His	Asp	Ile	
				90					95					100		
ggg	cat	ccg	ccg	tat	gga	cac	aac	ggt	gaa	aac	gcg	ttg	aat	gaa	gtt	451
Gly	His	Pro	Pro	Tyr	Gly	His	Asn	Gly	Glu	Asn	Ala	Leu	Asn	Glu	Val	
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gct gcg gcc tgt gga gga ttt gag ggc aac gcc caa acc ttg cgt att	499
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ctc acg cgt ctg gag cca aaa att gtc tct gat gag ggg gag agc ttt	547
Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp Glu Gly Glu Ser Phe	
135 140 145	
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Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala Ala Cys Lys Tyr Pro	
150 155 160 165	
tgg gct aaa aca aat gcg gat ggc agt gtc aat aag aaa tac agt gct	643
Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn Lys Lys Tyr Ser Ala	
170 175 180	
tat gac gag gac gca gaa atc ctc gct tgg att aga caa ggc cat gag	691
Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile Arg Gln Gly His Glu	
185 190 195	
gat ctt cgc cca ccg atc gaa gcg cag gtc atg gac ttt tct gat gac	739
Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met Asp Phe Ser Asp Asp	
200 205 210	
att gcc tac tcg gtg cac gat gtg gaa gac ggt att gta tcc ggg cgt	787
Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly Ile Val Ser Gly Arg	
215 220 225	
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Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu Leu Ala Ala Leu Ala	
230 235 240 245	
gac aaa gga gca gct gct ttc gga ggt tcg cct gca gag ctc atc gag	883
Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro Ala Glu Leu Ile Glu	
250 255 260	
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Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val Ala Ala Ala Asp	
265 270 275	
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Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu Lys Ala Met Thr Ser	
280 285 290	
gaa cta gtg gga aga tac gtt ggc tct acc atc gag tca aca aag aaa	1027
Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile Glu Ser Thr Lys Lys	
295 300 305	
aca cac gct ggc att gat gtg gga cgc atg cac ggc gat ttg atc att	1075
Thr His Ala Gly Ile Asp Val Gly Arg Met His Gly Asp Leu Ile Ile	
310 315 320 325	
cca gaa aca gcg gcc agt gaa gta aaa ctg ctc aaa acg tta gcg gtt	1123
Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu Lys Thr Leu Ala Val	
330 335 340	
ctc tac gtg atg gat gac cca ggg cac ctt gcg cgc caa aac agg caa	1171
Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala Arg Gln Asn Arg Gln	
345 350 355	
cgg gat cgt atc ttc cgg gtt ttt gac tac ctg gtg ctg ggg gct ccg	1219

Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu Val Leu Gly Ala Pro
 360 365 370

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 Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe Ile Glu Ala Asp Ser
 375 380 385

gaa tcg gaa cag atc cgt gtg att gtt gat cag att gcg tcg atg acg 1315
 Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln Ile Ala Ser Met Thr
 390 395 400 405

gag tct cgt ctg gaa cgc ctt gcc cgg aat gct gct gac atc tca gga 1363
 Glu Ser Arg Leu Glu Arg Leu Ala Arg Asn Ala Ala Asp Ile Ser Gly
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 Phe Leu Gly

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<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 1036

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Phe Ala Arg Asp Arg Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg
 35 40 45

Leu Ala Asp Lys Thr Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro
 50 55 60

Arg Thr Arg Leu Thr His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly
 65 70 75 80

Ile Gly Ala Gly Leu Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly
 85 90 95

Leu Cys His Asp Ile Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn
 100 105 110

Ala Leu Asn Glu Val Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala
 115 120 125

Gln Thr Leu Arg Ile Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp
 130 135 140

Glu Gly Glu Ser Phe Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala
 145 150 155 160

Ala Cys Lys Tyr Pro Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn
 165 170 175

Lys Lys Tyr Ser Ala Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile
 180 185 190

Arg Gln Gly His Glu Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met
 195 200 205
 Asp Phe Ser Asp Asp Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly
 210 215 220
 Ile Val Ser Gly Arg Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu
 225 230 235 240
 Leu Ala Ala Leu Ala Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro
 245 250 255
 Ala Glu Leu Ile Glu Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val
 260 265 270
 Ala Ala Ala Ala Asp Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu
 275 280 285
 Lys Ala Met Thr Ser Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile
 290 295 300
 Glu Ser Thr Lys Lys Thr His Ala Gly Ile Asp Val Gly Arg Met His
 305 310 315 320
 Gly Asp Leu Ile Ile Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu
 325 330 335
 Lys Thr Leu Ala Val Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala
 340 345 350
 Arg Gln Asn Arg Gln Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu
 355 360 365
 Val Leu Gly Ala Pro Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe
 370 375 380
 Ile Glu Ala Asp Ser Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln
 385 390 395 400
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 Ala Asp Ile Ser Gly Phe Leu Gly
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<210> 1037

<211> 1131

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1108)

<223> RXN01027

<400> 1037

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Asn	Lys	Pro	His	Glu	Val	Asp	Lys	Asp	Gln	Asp	Ser	Ala	Met	Leu	Ile		
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aac	ggc	cgc	ctg	caa	cag	atc	ccg	gcg	cgt	ccc	act	gag	gaa	ttc	acc	211	
Asn	Gly	Arg	Leu	Gln	Gln	Ile	Pro	Ala	Arg	Pro	Thr	Glu	Glu	Phe	Thr		
				25					30					35			
cgc	cca	act	ctt	gca	gca	ggc	gca	gta	ctg	tgg	cgc	ggc	gac	atc	acc	259	
Arg	Pro	Thr	Leu	Ala	Ala	Gly	Ala	Val	Leu	Trp	Arg	Gly	Asp	Ile	Thr		
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aac	ccg	gac	agc	atc	gag	gtc	gct	gtc	atc	cac	cgc	ccg	cac	tat	gat	307	
Asn	Pro	Asp	Ser	Ile	Glu	Val	Ala	Val	Ile	His	Arg	Pro	His	Tyr	Asp		
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gac	tgg	tcc	ctg	gcc	aag	ggc	aaa	gtc	gat	ccc	ggc	gag	tct	att	ccg	355	
Asp	Trp	Ser	Leu	Ala	Lys	Gly	Lys	Val	Asp	Pro	Gly	Glu	Ser	Ile	Pro		
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Thr	Thr	Ala	Ala	Arg	Glu	Ile	Leu	Glu	Glu	Thr	Gly	Tyr	Asp	Ile	Arg		
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ctg	ggc	aag	ctg	atc	ggc	aag	gtt	act	tac	cct	gtg	ctc	gac	cga	acc	451	
Leu	Gly	Lys	Leu	Ile	Gly	Lys	Val	Thr	Tyr	Pro	Val	Leu	Asp	Arg	Thr		
				105					110					115			
aaa	gtg	gtc	tac	tac	tgg	act	gcc	cag	gtt	ctt	ggc	gga	gag	ttt	gtc	499	
Lys	Val	Val	Tyr	Tyr	Trp	Thr	Ala	Gln	Val	Leu	Gly	Gly	Glu	Phe	Val		
				120					125					130			
ccc	aac	gat	gaa	gtt	gat	gaa	atc	cgt	tgg	ctg	tct	gtt	gat	gaa	gca	547	
Pro	Asn	Asp	Glu	Val	Asp	Glu	Ile	Arg	Trp	Leu	Ser	Val	Asp	Glu	Ala		
				135					140					145			
tgc	gag	ttg	ctc	agc	tac	caa	gta	gat	acc	gaa	gtt	ctg	gcc	aag	gca	595	
Cys	Glu	Leu	Leu	Ser	Tyr	Gln	Val	Asp	Thr	Glu	Val	Leu	Ala	Lys	Ala		
150					155					160					165		
gca	aag	cgt	ttc	cgc	act	cct	tcc	acc	act	cgg	gtg	ctg	tat	gtt	cgc	643	
Ala	Lys	Arg	Phe	Arg	Thr	Pro	Ser	Thr	Thr	Arg	Val	Leu	Tyr	Val	Arg		
				170					175					180			
cat	gct	cat	gca	cat	ggc	cgc	caa	acc	tgg	ggc	ggc	gac	gac	aat	aag	691	
His	Ala	His	Ala	His	Gly	Arg	Gln	Thr	Trp	Gly	Gly	Asp	Asp	Asn	Lys		
				185					190					195			
cgc	cca	ttg	gac	aaa	aag	ggg	cgt	cga	caa	gca	gaa	atg	ctc	gta	ccc	739	
Arg	Pro	Leu	Asp	Lys	Lys	Gly	Arg	Arg	Gln	Ala	Glu	Met	Leu	Val	Pro		
				200					205					210			
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Met	Leu	Leu</															

230	235	240	245	
gtg tcc gtc aac cga ctg ttc ggc gac gac gcc tgg gaa acc gat ccc				883
Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro	250	255	260	
gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa ggt ggc gtg				931
Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val	265	270	275	
ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg atc aaa tgg				979
Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp	280	285	290	
ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa				1027
Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys	295	300	305	
aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc				1075
Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly	310	315	320	325
gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg ttttaaggcct				1128
Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys	330	335		
cca				1131
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<213> Corynebacterium glutamicum				
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Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp	35	40	45	
Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His	50	55	60	
Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro	65	70	75	80
Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr	85	90	95	
Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro	100	105	110	
Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu	115	120	125	
Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu	130	135	140	

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
 145 150 155 160
 Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
 165 170 175
 Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
 180 185 190
 Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
 195 200 205
 Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr
 210 215 220
 Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp
 225 230 235 240
 Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala
 245 250 255
 Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val
 260 265 270
 Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro
 275 280 285
 Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu
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 Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp
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 Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
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<210> 1039

<211> 757

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> FRXA01024

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 Met Ala Asn Lys Asn
 1 5

aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc 163
 Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile
 10 15 20

aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211
 Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr
 25 30 35

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259
 Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr
 40 45 50

aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat 307
 Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp
 55 60 65

gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg 355
 Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro
 70 75 80 85

aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt 403
 Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg
 90 95 100

ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc 451
 Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr
 105 110 115

aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc 499
 Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val
 120 125 130

ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca 547
 Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala
 135 140 145

tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca 595
 Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala
 150 155 160 165

gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc 643
 Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg
 170 175 180

cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag 691
 His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys
 185 190 195

cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc 739
 Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro
 200 205 210

atg ttg ttg ccc ttc aaa 757
 Met Leu Leu Pro Phe Lys
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<210> 1040

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1040

Met Ala Asn Lys Asn Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp

1	5	10	15
Ser Ala Met	Leu Ile Asn Gly Arg	Leu Gln Gln Ile Pro	Ala Arg Pro
20		25	30
Thr Glu Glu	Phe Thr Arg Pro Thr	Leu Ala Ala Gly	Ala Val Leu Trp
35		40	45
Arg Gly Asp	Ile Thr Asn Pro Asp	Ser Ile Glu Val	Ala Val Ile His
50		55	60
Arg Pro His	Tyr Asp Asp Trp Ser	Leu Ala Lys Gly	Lys Val Asp Pro
65		70	75
Gly Glu Ser	Ile Pro Thr Thr	Ala Ala Arg	Glu Ile Leu Glu Glu Thr
	85	90	95
Gly Tyr Asp	Ile Arg Leu Gly Lys	Leu Ile Gly Lys	Val Thr Tyr Pro
	100	105	110
Val Leu Asp	Arg Thr Lys Val	Val Tyr Tyr Trp	Thr Ala Gln Val Leu
	115	120	125
Gly Gly Glu	Phe Val Pro Asn Asp	Glu Val Asp	Glu Ile Arg Trp Leu
	130	135	140
Ser Val Asp	Glu Ala Cys Glu Leu Leu	Ser Tyr Gln Val	Asp Thr Glu
145		150	155
Val Leu Ala	Lys Ala Ala Lys Arg	Phe Arg Thr Pro	Ser Thr Thr Arg
	165	170	175
Val Leu Tyr	Val Arg His Ala His	Ala His Gly Arg	Gln Thr Trp Gly
	180	185	190
Gly Asp Asp	Asn Lys Arg Pro	Leu Asp Lys Lys	Gly Arg Arg Gln Ala
	195	200	205
Glu Met Leu	Val Pro Met	Leu Leu Pro	Phe Lys
210		215	

<210> 1041

<211> 257

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(234)

<223> FRXA01027

<400> 1041

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Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln	
1 5 10 15	

ggg ggc gac atc att ccg gaa atg	96
Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met	
20 25 30	

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<210> 1042
<211> 78
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1042
Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln
  1          5          10          15
Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met
      20          25          30
Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile
      35          40          45
Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val
      50          55          60
Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
      65          70          75

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<210> 1043
<211> 651
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101) .. (628)  
<223> RXA01528
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<400> 1043
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gggtcgtagg tctccaacca ggaggcggtc caacacgagg gtg aat cag gcg tgg 115
                                         Val Asn Gln Ala Trp
                                         1                               5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163
Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu
                        10                        15                        20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211
Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp
                        25                        30                        35

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[illegible]

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<210> 1044
<211> 176
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1044
Val Asn Gln Ala Trp Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr
  1             5             10             15
Ser Ala Gly Gly Leu Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala
          20             25             30
Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg
          35             40             45
Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
  50             55             60
Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
  65             70             75             80

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<210> 1045
<211> 541
<212> DNA
<213> Corynebacterium glutamicum
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<400> 1045
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gtt aac gcc ctg aaa aat act ggt tcg gta aaa gat ccc gag atc tca 163
Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys Asp Pro Glu Ile Ser
10 15 20

ccc gaa gga cct cgc acg acc aca cgg ttg tca cca gag gta gca aaa 211
Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser Pro Glu Val Ala Lys
25 30 35

cat aac gag gaa ctc gtc gaa aag cat gct gct gcg ttg tat gac gcc 259
His Asn Glu Glu Leu Val Glu Lys His Ala Ala Ala Leu Tyr Asp Ala
40 45 50

agc gcg caa gag atc ctg gaa tgg aca gcc gag cac gcg ccg ggc gct 307
Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu His Ala Pro Gly Ala
 55 60 65

att gca gtg acc ttg agc atg gaa aac acc gtg ctg gcg gag ctg gct 355
Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu Ala Glu Leu Ala
70 75 80 85

gcg cgg cac ctg ccg gaa gct gat ttc ctc ttt ttg gac acc ggt tac 403
Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe Leu Asp Thr Gly Tyr

	90	95	100	
cac ttc aag gag acc ctt gaa gtt gcc cgt cag gta gat gag cgc tat				451
His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln Val Asp Glu Arg Tyr				
	105	110	115	
tcc cag aag ctt gtc acc gcg ctg ccg atc ctc aag cgc acg gag cag				499
Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu Lys Arg Thr Glu Gln				
	120	125	130	
gat tcc att tat ggt ctc aac ctg tac cgc agc aac cca gcg				541
Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser Asn Pro Ala				
	135	140	145	

<210> 1046

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 1046

Met Ser Phe Gln Leu Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys			
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Asp Pro Glu Ile Ser Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser			
20	25	30	
Pro Glu Val Ala Lys His Asn Glu Glu Leu Val Glu Lys His Ala Ala			
35	40	45	
Ala Leu Tyr Asp Ala Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu			
50	55	60	
His Ala Pro Gly Ala Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val			
65	70	75	80
Leu Ala Glu Leu Ala Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe			
85	90	95	
Leu Asp Thr Gly Tyr His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln			
100	105	110	
Val Asp Glu Arg Tyr Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu			
115	120	125	
Lys Arg Thr Glu Gln Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser			
130	135	140	
Asn Pro Ala			
145			

<210> 1047

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(979)

<223> RXA01878

<400> 1047

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atagtagaaa tctggcatcc aataggtaga ttgggatgct atg gaa gaa ccc tca 115
Met Glu Glu Pro Ser
1 5

ggg gca cag ctg ctc ggc ccg gta gaa atc cgt gcg ctg gca gaa aag 163
Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg Ala Leu Ala Glu Lys
10 15 20

ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat 211
Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln Asn Phe Val His Asp
25 30 35

ccc aac acg gtg cgt cgc att gtt gct gcg gca gag ctg acc cca aac 259
Pro Asn Thr Val Arg Arg Ile Val Ala Ala Glu Leu Thr Pro Asn
40 45 50

gac cac gtg gtg gaa gtt ggc cct ggt ctg ggc tct ctg acc ctt gcc 307
Asp His Val Val Glu Val Gly Pro Gly Leu Gly Ser Leu Thr Leu Ala
55 60 65

ctg gtg gaa tct gct gct tca gta act gcg gtg gaa att gat ccc cgt 355
Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val Glu Ile Asp Pro Arg
70 75 80 85

ttg gct gcg gaa ttg ccg gag act ttt cag tgg cgc gcg ccg gcc ctt 403
Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp Arg Ala Pro Ala Leu
90 95 100

gct cac aag ttg agc atc gtg ctg aaa gac gcc ctg aag gtt caa caa 451
Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala Leu Lys Val Gln Gln
105 110 115

tcc gat atg gct gtt caa ccc acc gcc ttg gtg gct aac ttg ccg tac 499
Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val Ala Asn Leu Pro Tyr
120 125 130

aac gtc tct gtc cct gtc ttg ttg cac atg atg gag gag ttt ccc acc 547
Asn Val Ser Val Pro Val Leu Leu His Met Met Glu Glu Phe Pro Thr
135 140 145

atc aac aag gtg ctt gtc atg gtg cag gca gag gtt gct gat cgt ttg 595
Ile Asn Lys Val Leu Val Met Val Gln Ala Glu Val Ala Asp Arg Leu
150 155 160 165

gct gcg gat cca gga tgc aag att tat ggt gtg cct agc gtg aag gcg 643
Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val Pro Ser Val Lys Ala
170 175 180

tcc ttc tac ggt cca gtt act cgc gcc ggg tgc att ggt aag aat gtc 691
Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser Ile Gly Lys Asn Val
185 190 195

ttt tgg cca gct cca aag atc gaa tcc ggt ttg gtg aag atc gtg cgc 739
Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu Val Lys Ile Val Arg
200 205 210

gaa gac acc gcg tgg aag cag gac gat gag acg cgt aag aag gtg tgg 787

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Glu	Asp	Thr	Ala	Trp	Lys	Gln	Asp	Asp	Glu	Thr	Arg	Lys	Lys	Val	Trp		
215						220					225						
ccg	atc	att	gat	gct	gct	ttc	ttg	cag	cgc	cgt	aaa	acc	cta	aga	gct	835	
Pro	Ile	Ile	Asp	Ala	Ala	Phe	Leu	Gln	Arg	Arg	Lys	Thr	Leu	Arg	Ala		
230					235					240					245		
gcg	ctt	tct	gga	cac	tac	ggg	tct	ggc	cag	gca	gct	gag	gaa	gct	ttg	883	
Ala	Leu	Ser	Gly	His	Tyr	Gly	Ser	Gly	Gln	Ala	Ala	Glu	Glu	Ala	Leu		
				250					255					260			
cgg	gcc	gct	gat	att	gat	cca	acg	ctt	cgt	ggc	gaa	aag	ctt	gat	gtc	931	
Arg	Ala	Ala	Asp	Ile	Asp	Pro	Thr	Leu	Arg	Gly	Glu	Lys	Leu	Asp	Val		
			265					270						275			
act	gac	tat	gtg	cgc	cta	gct	ggg	gtg	ttg	cag	caa	aag	gat	gag	aag	979	
Thr	Asp	Tyr	Val	Arg	Leu	Ala	Gly	Val	Leu	Gln	Gln	Lys	Asp	Glu	Lys		
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<210> 1048

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 1048

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Ala	Leu	Ala	Glu	Lys	Leu	Asp	Val	Thr	Pro	Thr	Lys	Lys	Leu	Gly	Gln		
			20					25					30				
Asn	Phe	Val	His	Asp	Pro	Asn	Thr	Val	Arg	Arg	Ile	Val	Ala	Ala	Ala		
		35					40					45					
Glu	Leu	Thr	Pro	Asn	Asp	His	Val	Val	Glu	Val	Gly	Pro	Gly	Leu	Gly		
	50					55					60						
Ser	Leu	Thr	Leu	Ala	Leu	Val	Glu	Ser	Ala	Ala	Ser	Val	Thr	Ala	Val		
	65				70				75						80		
Glu	Ile	Asp	Pro	Arg	Leu	Ala	Ala	Glu	Leu	Pro	Glu	Thr	Phe	Gln	Trp		
				85					90					95			
Arg	Ala	Pro	Ala	Leu	Ala	His	Lys	Leu	Ser	Ile	Val	Leu	Lys	Asp	Ala		
			100					105					110				
Leu	Lys	Val	Gln	Gln	Ser	Asp	Met	Ala	Val	Gln	Pro	Thr	Ala	Leu	Val		
		115					120					125					
Ala	Asn	Leu	Pro	Tyr	Asn	Val	Ser	Val	Pro	Val	Leu	Leu	His	Met	Met		
	130					135					140						
Glu	Glu	Phe	Pro	Thr	Ile	Asn	Lys	Val	Leu	Val	Met	Val	Gln	Ala	Glu		
	145				150					155					160		
Val	Ala	Asp	Arg	Leu	Ala	Ala	Asp	Pro	Gly	Ser	Lys	Ile	Tyr	Gly	Val		
				165					170					175			

Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser
 180 185 190

Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu
 195 200 205

Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr
 210 215 220

Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg
 225 230 235 240

Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala
 245 250 255

Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly
 260 265 270

Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln
 275 280 285

Gln Lys Asp Glu Lys
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<210> 1049

<211> 1545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXN02281

<400> 1049

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cctataaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115
 Val Gln Lys Asp Ser
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg
 70 75 80 85

gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat	403
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn	
90 95 100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg	451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro	
105 110 115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt	499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly	
120 125 130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac	547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp	
135 140 145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg	595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro	
150 155 160 165	
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc	643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile	
170 175 180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg	691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu	
185 190 195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg	739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met	
200 205 210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca	787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro	
215 220 225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa	835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu	
230 235 240 245	
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc	883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	
250 255 260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca	931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	
265 270 275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa	979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	
280 285 290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc	1027
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	
295 300 305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att	1075
Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile	
310 315 320 325	

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa 1123
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 330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac 1171
 Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp
 345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac 1219
 Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn
 360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc 1267
 Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser
 375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga 1315
 Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly
 390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg 1363
 Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu
 410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac 1411
 Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr
 425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa 1459
 Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu
 440 445 450

tac ctg gca gta gat cct gaa ccg ttg cgt acc cgt aaa ctg cgc agg 1507
 Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg
 455 460 465

acc ttg ggt gag gtg ccg ttt cgc taaagtctcg gaga 1545
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<210> 1050

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 1050

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Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala
 20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
 35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
 50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80

Leu	Ser	Lys	Pro	Arg 85	Val	Ile	Glu	Arg	Tyr 90	Leu	Arg	Glu	Gln	Leu 95	Glu
Arg	Leu	Thr	Ser 100	Asn	Tyr	Pro	Cys	Lys 105	Ile	Tyr	Val	Ser	Glu 110	Ser	Asp
Ile	Arg	Ile 115	Pro	Pro	Glu	Tyr	Ile 120	Arg	Gly	Ala	Pro	Ser 125	Ala	Thr	Glu
Ala	Arg 130	Arg	Ala	Gly	Asp	Val 135	Ala	Asp	Ile	Ile	Pro 140	Arg	Pro	Thr	Leu
Asp 145	Glu	Val	His	Asp	Ala 150	Ile	Ile	Asp	Gly	Asp 155	Trp	His	Ala	Phe	Asn 160
Gly	Pro	Glu	Leu 165	Pro	Leu	Phe	His	Phe	Gly 170	Pro	Gln	Arg	Phe	Asp 175	Ile
Ala	Cys	Ala	Arg 180	Ile	Glu	His	Tyr	Thr 185	Gly	Ile	Asn	Val	Glu 190	His	Val
Gln	Lys	Tyr 195	Ile	Leu	Phe	Thr	Asn 200	Tyr	Ala	Met	His	Thr 205	Thr	Glu	Phe
Val	His 210	Phe	Ala	Met	Ser	Glu 215	Leu	Thr	Ser	Glu	Asp 220	Ser	Arg	Tyr	Val
Gly 225	Leu	Ser	Leu	Pro	Asn 230	Gly	Gln	Val	Ile	Asp 235	Arg	Glu	Thr	Ala	Thr 240
Ser	Leu	Gly	Thr	Glu 245	Thr	Leu	Asp	Leu	Thr 250	Ser	Arg	Phe	Gln	Met 255	Pro
Arg	Tyr	Asp	Leu 260	Ile	Thr	Glu	Ala	Gly 265	Asp	Gly	Ile	Thr	Ile 270	Ile	Asn
Ile	Gly	Val 275	Gly	Pro	Ser	Asn	Ala 280	Lys	Thr	Ile	Thr	Asp 285	Cys	Leu	Ala
Val 290	Leu	Arg	Pro	Glu	Ala	Trp 295	Val	Met	Ile	Gly	His 300	Cys	Ala	Gly	Met
Asp 305	Ala	Arg	Met	Arg	Ile 310	Gly	Asp	Leu	Ile	Leu 315	Gly	Asn	Ala	Tyr	Gln 320
Arg	Glu	Asp	His	Ile 325	Leu	Asn	Thr	Arg	Ile 330	Pro	Leu	Gly	Asn	Pro 335	Ile
Pro	Ala	Ile 340	Pro	Glu	Ile	Gln	Lys	Ala 345	Leu	Glu	Ala	Ser	Val 350	Asp	Glu
Ile	Tyr	Gly 355	Ser	Asp	Asn	Ser	Leu	Met	Arg	Thr	Gly	Thr 365	Val	Leu	Ser
Thr 370	Asp	Asp	Arg	Asn	Trp	Glu 375	Trp	His	Thr	Pro	Glu 380	Asn	Leu	Trp	Asn
Trp 385	Leu	Lys	Gly	Ser	Thr 390	Ala	Ala	Ala	Val	Asp 395	Met	Glu	Ser	Ser	Thr 400

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<210> 1051
<211> 1191
<212> DNA
<213> Corynebacterium glutamicum
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<400> 1051																
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Val Gln Lys Asp Ser 5																
gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163																
Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu 20																
att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211																
Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn 30 35																
aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259																
Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr 40 45 50																
gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307																
Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly 55 60 65																
tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355																
Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg 70 75 80 85																
gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403																
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn 90 95 100																
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg 451																
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro 105 110 115																

gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt	499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly	
120 125 130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac	547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp	
135 140 145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg	595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro	
150 155 160 165	
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc	643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile	
170 175 180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg	691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu	
185 190 195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg	739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met	
200 205 210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca	787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro	
215 220 225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa	835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu	
230 235 240 245	
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc	883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	
250 255 260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca	931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	
265 270 275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa	979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	
280 285 290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc	1027
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	
295 300 305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att	1075
Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile	
310 315 320 325	
ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa	1123
Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu	
330 335 340	
atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc	1168
Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser	
345 350 355	
tagtattcta tagtgtcacc taa	1191

<210> 1052

<211> 356

<212> PRT

<213> Corynebacterium glutamicum

<400> 1052

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp
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Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala
 20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
 35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
 50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
 85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
 100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
 115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
 130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
 145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
 165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
 180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
 195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
 210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240

Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255

Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270

Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285

Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300

Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320

Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
 325 330 335

Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350

Ile Tyr Gly Ser
 355

<210> 1053

<211> 1146

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1123)

<223> RXN01240

<400> 1053

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ctgcacagga aagtttagcgg cgctactatg aacgatcgat atg tct gac aac act 115
 Met Ser Asp Asn Thr
 1 5

ctc tcc caa ttt ggc agt tac tac cac gaa ttc cga cgt gcc cat ccc 163
 Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe Arg Arg Ala His Pro
 10 15 20

atg gcc gac gtc gaa ttc ctc cta gca att gaa gaa tta ctt acg gac 211
 Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu Glu Leu Leu Thr Asp
 25 30 35

ggg ggt gtc acc ttc gat cgc gtc acc aca cgc atc aaa gaa tgg tca 259
 Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg Ile Lys Glu Trp Ser
 40 45 50

agc ctg aaa gcc aag gct cgc aag cgt cgc aac gat ggc tcg ttg atc 307
 Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn Asp Gly Ser Leu Ile
 55 60 65

tac cct gat ccg cgc aaa gac atc cac gac atg atc ggt gtt cgg atc 355
 Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met Ile Gly Val Arg Ile
 70 75 80 85

acc acg tac cac tcc acg gaa ata ccc gtg gcc cta aaa gtg ctc caa 403
 Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala Leu Lys Val Leu Gln
 90 95 100

gac tcc ttc atc gtc cac aaa tcc gta gac aaa gcc gct gaa act cgc 451
 Asp Ser Phe Ile Val His Lys Ser Val Asp Lys Ala Ala Glu Thr Arg
 105 110 115

atc tca ggc ggc ttt ggt tac ggc tcc cac cac ctg att ctg gaa gtc 499
 Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His Leu Ile Leu Glu Val
 120 125 130

gat gac acc tcc gat gac ctc cag gac tac aaa ggc ctc gtc ttt gaa 547
 Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys Gly Leu Val Phe Glu
 135 140 145

gtt cag gtg cgc acc gtg ctg caa cac gcc tgg gca gag ttc gaa cac 595
 Val Gln Val Arg Thr Val Leu Gln His Ala Trp Ala Glu Phe Glu His
 150 155 160 165

gat atc cgc tat aaa cgc gcc gat gtg tcc aac cca gaa gac ttc agc 643
 Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn Pro Glu Asp Phe Ser
 170 175 180

gca gaa gta gac cgc atg ttc acc ctc gct gcc gga ctc atc gaa tta 691
 Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala Gly Leu Ile Glu Leu
 185 190 195

gcg gac caa caa ttc gac caa atc gcc gca ctc aaa gaa acc agc cga 739
 Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu Lys Glu Thr Ser Arg
 200 205 210

gtt gct gat gaa tcc gtc gaa ctc acc gca gag aca ctt ccc ggc gtt 787
 Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu Thr Leu Pro Gly Val
 215 220 225

ctt gcc atg ctc att ggc aac cgc ttc ccc cgc cca cgc tcc aca aac 835
 Leu Ala Met Leu Ile Gly Asn Arg Phe Pro Arg Pro Arg Ser Thr Asn
 230 235 240 245

tac cgc ttc ctc gaa gac atc ctg gtg gcc aac tcc att acc tct gtg 883
 Tyr Arg Phe Leu Glu Asp Ile Leu Val Ala Asn Ser Ile Thr Ser Val
 250 255 260

gtg cag ctg cgc gag ctg ctc aac ccc acc gac att gaa gtg ctg ttg 931
 Val Gln Leu Arg Glu Leu Leu Asn Pro Thr Asp Ile Glu Val Leu Leu
 265 270 275

aaa gta atg aac tac cgc ttc cac cca ggc cag atc cgc atc atc gac 979
 Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln Ile Arg Ile Ile Asp
 280 285 290

gat tta cta ctc aaa cga ttt ggc caa tca cac atc gat gcc acc gtc 1027
 Asp Leu Leu Leu Lys Arg Phe Gly Gln Ser His Ile Asp Ala Thr Val
 295 300 305

gcc acc gac tcc caa cca ctc aac gcc aaa cgc cac agg cag cta aaa 1075
 Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg His Arg Gln Leu Lys
 310 315 320 325

cgc aag cta gag ctc atg acc caa gct cat ctt gtg gaa cca cca aac 1123
 Arg Lys Leu Glu Leu Met Thr Gln Ala His Leu Val Glu Pro Pro Asn
 330 335 340

taaagttccc ccaaagtttag ccc 1146

<210> 1054

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 1054

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Met Ser Asp Asn Thr Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe
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Arg Arg Ala His Pro Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu
          20           25           30

Glu Leu Leu Thr Asp Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg
          35           40           45

Ile Lys Glu Trp Ser Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn
          50           55           60

Asp Gly Ser Leu Ile Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met
          65           70           75           80

Ile Gly Val Arg Ile Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala
          85           90           95

Leu Lys Val Leu Gln Asp Ser Phe Ile Val His Lys Ser Val Asp Lys
          100          105          110

Ala Ala Glu Thr Arg Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His
          115          120          125

Leu Ile Leu Glu Val Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys
          130          135          140

Gly Leu Val Phe Glu Val Gln Val Arg Thr Val Leu Gln His Ala Trp
          145          150          155          160

Ala Glu Phe Glu His Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn
          165          170          175

Pro Glu Asp Phe Ser Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala
          180          185          190

Gly Leu Ile Glu Leu Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu
          195          200          205

Lys Glu Thr Ser Arg Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu
          210          215          220

Thr Leu Pro Gly Val Leu Ala Met Leu Ile Gly Asn Arg Phe Pro Arg
          225          230          235          240

Pro Arg Ser Thr Asn Tyr Arg Phe Leu Glu Asp Ile Leu Val Ala Asn
          245          250          255

Ser Ile Thr Ser Val Val Gln Leu Arg Glu Leu Leu Asn Pro Thr Asp
          260          265          270

Ile Glu Val Leu Leu Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln
          275          280          285

Ile Arg Ile Ile Asp Asp Leu Leu Leu Lys Arg Phe Gly Gln Ser His
          290          295          300

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Ile Asp Ala Thr Val Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg
305 310 315 320

His Arg Gln Leu Lys Arg Lys Leu Glu Leu Met Thr Gln Ala His Leu
325 330 335

Val Glu Pro Pro Asn
340

<210> 1055

<211> 1234

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1234)

<223> RXN02008

<400> 1055

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Val Tyr Ala Ala Ile
1 5

ggt gtc gtg cac tcc ctg ttc aat gct ctg cct ggc cga ttc aaa gac 163
Gly Val Val His Ser Leu Phe Asn Ala Leu Pro Gly Arg Phe Lys Asp
10 15 20

tat att tca gcc ccg cgc ttc ggt gtc tac caa tcc ctg cac acc acc 211
Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln Ser Leu His Thr Thr
25 30 35

gtg atg gga cct ggc ggt aag cct ctg gaa gtt cag gca cgt acc cac 259
Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val Gln Ala Arg Thr His
40 45 50

gac atg cac tac aac gcc gaa ttc ggc att gca gcg cac tgg cga tac 307
Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala Ala His Trp Arg Tyr
55 60 65

aaa gaa acc aaa ggc agc cac agt ggc gag caa gcc gaa gtg gat caa 355
Lys Glu Thr Lys Gly Ser His Ser Gly Glu Gln Ala Glu Val Asp Gln
70 75 80 85

atg gcg tgg atg cgc caa ctt ctg gac tgg caa aaa gaa gca gcc gac 403
Met Ala Trp Met Arg Gln Leu Leu Asp Trp Gln Lys Glu Ala Ala Asp
90 95 100

ccc aac gag ttc ctg gac agc ctg cgc tac gat ctg act tcc aag cag 451
Pro Asn Glu Phe Leu Asp Ser Leu Arg Tyr Asp Leu Thr Ser Lys Gln
105 110 115

atc ttc gtg ttc aca ccc aaa ggt gat gtg gtc aac ctg ccg gtg aac 499
Ile Phe Val Phe Thr Pro Lys Gly Asp Val Val Asn Leu Pro Val Asn
120 125 130

tcc acc ccg gtg gac ttc gcc tac gcg gtg cac acc gaa gtg ggg cac 547

[illegible]

375

<210> 1056

<211> 378

<212> PRT

<213> Corynebacterium glutamicum

<400> 1056

Val	Tyr	Ala	Ala	Ile	Gly	Val	Val	His	Ser	Leu	Phe	Asn	Ala	Leu	Pro
1				5					10					15	

Gly	Arg	Phe	Lys	Asp	Tyr	Ile	Ser	Ala	Pro	Arg	Phe	Gly	Val	Tyr	Gln
			20					25					30		

Ser	Leu	His	Thr	Thr	Val	Met	Gly	Pro	Gly	Gly	Lys	Pro	Leu	Glu	Val
		35					40					45			

Gln	Ala	Arg	Thr	His	Asp	Met	His	Tyr	Asn	Ala	Glu	Phe	Gly	Ile	Ala
	50					55					60				

Ala	His	Trp	Arg	Tyr	Lys	Glu	Thr	Lys	Gly	Ser	His	Ser	Gly	Glu	Gln
	65				70					75					80

Ala	Glu	Val	Asp	Gln	Met	Ala	Trp	Met	Arg	Gln	Leu	Leu	Asp	Trp	Gln
				85					90					95	

Lys	Glu	Ala	Ala	Asp	Pro	Asn	Glu	Phe	Leu	Asp	Ser	Leu	Arg	Tyr	Asp
			100					105					110		

Leu	Thr	Ser	Lys	Gln	Ile	Phe	Val	Phe	Thr	Pro	Lys	Gly	Asp	Val	Val
		115					120					125			

Asn	Leu	Pro	Val	Asn	Ser	Thr	Pro	Val	Asp	Phe	Ala	Tyr	Ala	Val	His
	130					135					140				

Thr	Glu	Val	Gly	His	Arg	Cys	Ile	Gly	Ala	Lys	Ile	Asn	Gly	Lys	Leu
145					150					155					160

Val	Ala	Leu	Glu	Thr	Lys	Leu	Lys	Ser	Gly	Asp	Arg	Val	Glu	Val	Phe
				165					170					175	

Thr	Ser	Lys	Asp	Gln	Asn	Ala	Gly	Pro	Ser	Arg	Gly	Trp	Gln	Glu	Phe
			180					185					190		

Val	Val	Ser	Pro	Arg	Ala	Lys	Ala	Lys	Ile	Arg	Gln	Trp	Phe	Ala	Lys
		195					200					205			

Glu	Arg	Arg	Glu	Glu	Tyr	Leu	Glu	Ala	Gly	Arg	Asp	Ala	Leu	Ala	Ala
	210					215					220				

Val	Ile	Gln	Arg	Gly	Gly	Leu	Pro	Met	His	Arg	Leu	Phe	Thr	Ala	Ser
225					230					235					240

Ser	Met	Lys	Thr	Val	Ala	Thr	Glu	Leu	His	Tyr	Pro	Asp	Val	Asp	Ala
				245					250					255	

Leu	Tyr	Thr	Ala	Ile	Gly	Ser	Gly	Ser	Val	Ser	Ala	Gln	His	Val	Val
			260					265					270		

Asn	Arg	Leu	Met	Ala	Ile	Phe	Gly	Asp	Glu	Glu	Asp	Ala	Glu	Asp	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

275					280					285					
Leu	Val	Ala	Arg	Thr	Pro	Phe	Ser	Glu	Leu	Val	Asn	Ser	Arg	Ala	Thr
290					295					300					
Thr	Glu	Ser	Ser	Thr	Gly	Ile	Leu	Val	Glu	Gly	Ser	Pro	Asp	Val	Met
305					310					315					320
Ala	Lys	Leu	Ala	Lys	Cys	Cys	Met	Pro	Val	Pro	Gly	Asp	Glu	Ile	Phe
				325					330					335	
Gly	Phe	Val	Thr	Arg	Gly	Gly	Gly	Val	Ser	Val	His	Arg	Thr	Asp	Cys
			340					345					350		
Thr	Asn	Val	Glu	Lys	Leu	Lys	Glu	Glu	Pro	Glu	Arg	Ile	Val	Ser	Val
		355					360					365			
Ser	Trp	Ala	Ser	Glu	Gly	Gln	Gly	Ser	Val						
	370					375									

<210> 1057

<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> RXN01940

<400> 1057

ccagaatcaa tcaccgatac agtggcagcc aaagtccagg ctgaagaagc cgctcaagcc 60

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gccagctaaa tccacaaact gaactaagga gttttaccct atg acc acc aag atc    115
                    Met Thr Thr Lys Ile
                               1                5

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atc ctc gac tgc gat cca gga cac gac gac gct gta gcc atg ctg ctc    163
Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala Val Ala Met Leu Leu
                    10                15                20

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```

gca gcc ggc agc cca gaa att gaa ctg ctt gga atc acc acg gtc ggc    211
Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly Ile Thr Thr Val Gly
                    25                30                35

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ggc aac cag acc ttg gac aag gtc acc cac aat acg cag gtc gta gcc    259
Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn Thr Gln Val Val Ala
                    40                45                50

```

```

acc atc gct gat atc aat gcg ccc atc tac cgc ggt gtc acc cga cca    307
Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg Gly Val Thr Arg Pro
                    55                60                65

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```

ttg gtg cgc ccc gtt gag gta gcc gaa gat atc cac ggc gat acc ggc    355
Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile His Gly Asp Thr Gly
                    70                75                80                85

```

```

atg gaa atc cac aag tac gaa ctg cct gaa cca acc aag cag gta gaa    403
Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro Thr Lys Gln Val Glu
                    90                95                100

```

gac acc cac gcg gtg gat ttc atc atc gat acc atc atg aat aac gag 451
 Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr Ile Met Asn Asn Glu
 105 110 115

ccc gcc agc gta gcg ctg gtt ccc acc gga cca ctg acc aac atc gcg 499
 Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro Leu Thr Asn Ile Ala
 120 125 130

ctg gca gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt 547
 Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val
 135 140 145

gtc ctc atg gcc ggg gcc tac cac gta gga aac tgg acc gcc gta gct 595
 Val Leu Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala
 150 155 160 165

gaa ttc aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac 643
 Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn
 170 175 180

gaa aag tgg cca ctg act atg gtc gcc ctc gac ctt acc cac cag gcg 691
 Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala
 185 190 195

ctc gca aca cct gag atc gaa gcc aag ttc aac gag ctg gcc acc gac 739
 Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp
 200 205 210

gtc gcc gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac 787
 Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr
 215 220 225

cag gac gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct 835
 Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala
 230 235 240 245

gtt gca tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca 883
 Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro
 250 255 260

ctc gat gtg gag ctg tac gcc gca ctc acc aca gcc atg acc gtt gct 931
 Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala
 265 270 275

gat ttc cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt 979
 Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val
 280 285 290

gac ctg gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag 1027
 Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys
 295 300 305

cgc atc gga tagacctgtt cacaaggttg tta 1059
 Arg Ile Gly
 310

<210> 1058

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 1058

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Met Thr Thr Lys Ile Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala
 1           5           10           15

Val Ala Met Leu Leu Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly
      20           25           30

Ile Thr Thr Val Gly Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn
      35           40           45

Thr Gln Val Val Ala Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg
      50           55           60

Gly Val Thr Arg Pro Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile
      65           70           75           80

His Gly Asp Thr Gly Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro
      85           90           95

Thr Lys Gln Val Glu Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr
      100           105           110

Ile Met Asn Asn Glu Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro
      115           120           125

Leu Thr Asn Ile Ala Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu
      130           135           140

Arg Val Lys Glu Val Val Leu Met Gly Gly Gly Tyr His Val Gly Asn
      145           150           155           160

Trp Thr Ala Val Ala Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala
      165           170           175

His Ile Val Phe Asn Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp
      180           185           190

Leu Thr His Gln Ala Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn
      195           200           205

Glu Leu Gly Thr Asp Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala
      210           215           220

Phe Arg Lys Asn Tyr Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val
      225           230           235           240

His Asp Pro Cys Ala Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr
      245           250           255

Thr Arg Lys Ala Pro Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr
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Gly Met Thr Val Ala Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr
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305

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<220>

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<223> FRXA01940

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Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu	
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atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct gaa ttc	144
Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe	
35 40 45	
aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac gaa aag	192
Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys	
50 55 60	
tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg ctc gca	240
Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala	
65 70 75 80	
aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac gtc gcc	288
Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala	
85 90 95	
gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac cag gac	336
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp	
100 105 110	
gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct gtt gca	384
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala	
115 120 125	
tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca ctc gat	432
Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp	
130 135 140	
gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct gat ttc	480
Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe	
145 150 155 160	
cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt gac ctg	528
Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu	
165 170 175	
gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag cgc atc	576
Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile	
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Gly

602

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35 40 45
Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys
50 55 60
Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala
65 70 75 80
Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala
85 90 95
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp
100 105 110
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala
115 120 125
Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp
130 135 140
Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe
145 150 155 160
Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu
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Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile
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Gly

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<220>
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<223> RXA02559

<400> 1061

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                                         Met Ile Pro Val Leu
                                         1                               5

atc gac tgc gac acc ggc atc gac gac gcc ctc gcc ctg atc tac ctg 163
Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ile Tyr Leu
                               10                               15                               20

gtt gct ttg cat aaa cgt ggt gaa atc caa ctt ttt gga gca acg acc 211
Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu Phe Gly Ala Thr Thr
                               25                               30                               35

acc gca gga aat gtt gat gtg aaa caa acc gcc atc aat acc agg tgg 259
Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala Ile Asn Thr Arg Trp
                               40                               45                               50

gtg ttg gat cag tgt gga tta gcg gac atc ccg gtc ctc gca gga caa 307
Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro Val Leu Ala Gly Gln
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cct gaa cca aag cac gtg ccg cta gtg act act cca gaa aca cac ggc 355
Pro Glu Pro Lys His Val Pro Leu Val Thr Thr Pro Glu Thr His Gly
                               70                               75                               80                               85

gac cat ggc ctt ggt tat ata aac cca ggt cac gtc gaa att cca gaa 403
Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His Val Glu Ile Pro Glu
                               90                               95                               100

ggg gac tgg aag cag ctg tgg aaa gaa cac ctc agt aac cca gaa act 451
Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu Ser Asn Pro Glu Thr
                               105                               110                               115

aag ctg att gtc acc ggg ccc gcc acc aac ctt gcg gaa ttc ggg cca 499
Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu Ala Glu Phe Gly Pro
                               120                               125                               130

gtg gaa aac gtc acg ctg atg ggt ggc acc tac ctt tat cca ggc aac 547
Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr Leu Tyr Pro Gly Asn
                               135                               140                               145

acc act cca acg gca gaa tgg aat acc tgg gtt gat cca cac gga gct 595
Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val Asp Pro His Gly Ala
                               150                               155                               160                               165

aaa gaa gca ttc gcg gca gcc caa aag ccc att acg gtg tgt tcc ttg 643
Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile Thr Val Cys Ser Leu
                               170                               175                               180

ggc gtg acc gag cag ttt acg ctg aac ccg gac atc ctt tct aca ctt 691
Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp Ile Leu Ser Thr Leu
                               185                               190                               195

atc aac acg ctt ggc agc caa ccc atc gca gag cat tta cct gag atg 739
Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu His Leu Pro Glu Met
                               200                               205                               210

ctg cgc ttt tac ttt gaa ttt cac gaa gtg cag ggc gaa ggt tac ctt 787

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Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln Gly Glu Gly Tyr Leu
 215 220 225
 gct caa att cat gac ctg ctg acc tgc atg att gcc ttg gat aaa atc 835
 Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile Ala Leu Asp Lys Ile
 230 235 240 245
 cca ttt tca ggc cgt gaa gta acc gtg gac gtg gag gct gat tcg ccc 883
 Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val Glu Ala Asp Ser Pro
 250 255 260
 ttg atg cgt ggc acc act gtt gca gat att cgc gga cat tgg ggc aag 931
 Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg Gly His Trp Gly Lys
 265 270 275
 cca gct aac gca ttt ctt gtg gaa acc gca gac att gag gcc gcc cac 979
 Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp Ile Glu Ala Ala His
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 gcg gaa ctt cta aga gca gtg gaa tgaaataatc cgggtgctgat gca 1026
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 Phe Gly Ala Thr Thr Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala
 35 40 45
 Ile Asn Thr Arg Trp Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro
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 Val Leu Ala Gly Gln Pro Glu Pro Lys His Val Pro Leu Val Thr Thr
 65 70 75 80
 Pro Glu Thr His Gly Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His
 85 90 95
 Val Glu Ile Pro Glu Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu
 100 105 110
 Ser Asn Pro Glu Thr Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu
 115 120 125
 Ala Glu Phe Gly Pro Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr
 130 135 140
 Leu Tyr Pro Gly Asn Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val
 145 150 155 160
 Asp Pro His Gly Ala Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile

165										170					175				
Thr	Val	Cys	Ser	Leu	Gly	Val	Thr	Glu	Gln	Phe	Thr	Leu	Asn	Pro	Asp				
			180					185					190						
Ile	Leu	Ser	Thr	Leu	Ile	Asn	Thr	Leu	Gly	Ser	Gln	Pro	Ile	Ala	Glu				
		195					200					205							
His	Leu	Pro	Glu	Met	Leu	Arg	Phe	Tyr	Phe	Glu	Phe	His	Glu	Val	Gln				
		210				215					220								
Gly	Glu	Gly	Tyr	Leu	Ala	Gln	Ile	His	Asp	Leu	Leu	Thr	Cys	Met	Ile				
225					230					235					240				
Ala	Leu	Asp	Lys	Ile	Pro	Phe	Ser	Gly	Arg	Glu	Val	Thr	Val	Asp	Val				
			245						250					255					
Glu	Ala	Asp	Ser	Pro	Leu	Met	Arg	Gly	Thr	Thr	Val	Ala	Asp	Ile	Arg				
			260					265					270						
Gly	His	Trp	Gly	Lys	Pro	Ala	Asn	Ala	Phe	Leu	Val	Glu	Thr	Ala	Asp				
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Ile	Glu	Ala	Ala	His	Ala	Glu	Leu	Leu	Arg	Ala	Val	Glu							
	290					295					300								

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<212> DNA

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<222> (101)..(1027)

<223> RXA02497

<400> 1063

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				Val	Arg	Leu	Gly	Val	
				1				5	

tta	gat	gtg	ggc	agc	aat	act	gtc	cac	cta	ggt	gca	gta	gac	gcg	cgt	163
Leu	Asp	Val	Gly	Ser	Asn	Thr	Val	His	Leu	Val	Ala	Val	Asp	Ala	Arg	
			10					15					20			

ccc	ggt	gga	cac	ccc	acc	ccg	atg	agc	aat	tgg	cgt	acc	cca	ctg	cgc	211
Pro	Gly	Gly	His	Pro	Thr	Pro	Met	Ser	Asn	Trp	Arg	Thr	Pro	Leu	Arg	
			25					30					35			

ctt	ggt	gag	ctt	ctt	gat	gac	tcc	ggg	gcg	atc	tcc	gaa	aag	ggc	atc	259
Leu	Val	Glu	Leu	Leu	Asp	Asp	Ser	Gly	Ala	Ile	Ser	Glu	Lys	Gly	Ile	
		40				45						50				

aac	aaa	ctc	acc	tca	gca	gtc	ggg	gaa	gca	gca	gac	cta	gcg	aaa	acg	307
Asn	Lys	Leu	Thr	Ser	Ala	Val	Gly	Glu	Ala	Ala	Asp	Leu	Ala	Lys	Thr	
	55					60					65					

ctc	ggc	tgc	gct	gaa	ctg	atg	cca	ttt	gct	aca	tcg	gca	gtc	cgc	tcc	355
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<211> 309

<212> PRT

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10

15

Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp

20

25

30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile

35

40

45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala

50

55

60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr

65

70

75

80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val

85

90

95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu

100

105

110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala

115

120

125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser

130

135

140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly

145

150

155

160

Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg

165

170

175

Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu

180

185

190

Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly

195

200

205

Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro

210

215

220

Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu

225

230

235

240

Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala

245

250

255

Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly

260

265

270

Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val

275

280

285

Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile
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Asp Lys Gly Leu Glu
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<210> 1065

<211> 2226

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(2203)

<223> RXN01079

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 Met Asp Phe His Ala
 1 5

ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163
 Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe
 10 15 20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211
 Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn
 25 30 35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259
 Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu Lys Ile Asp Tyr Leu
 40 45 50

gtt gaa aac aag tac tat gac cca atc gtt ctg gac aag tac gac ttc 307
 Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu Asp Lys Tyr Asp Phe
 55 60 65

cag ttc atc aag gac ctc ttc aag cgc gca tac gga ttc aag ttc cgc 355
 Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr Gly Phe Lys Phe Arg
 70 75 80 85

ttc cag tcc ttc ctc ggt gca tac aag tac tac act tcc tac acc ctg 403
 Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr Thr Ser Tyr Thr Leu
 90 95 100

aag acc ttc gac ggt cgc cgc tac ctc gag cgt ttc gaa gac cgt gtc 451
 Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg Phe Glu Asp Arg Val
 105 110 115

tgc atg gtc gcc ctc acc ctc gct gac ggc gac cgc gca ttg gcc gag 499
 Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp Arg Ala Leu Ala Glu
 120 125 130

aac ctg gtc gat gag atc atg tct ggc cgt ttc caa cca gca acc cca 547
 Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe Gln Pro Ala Thr Pro
 135 140 145

acc ttc ctg aac tcc ggc aag gca cag cgc ggc gag cca gta tcc tgc 595

Thr 150	Phe	Leu	Asn	Ser	Gly 155	Lys	Ala	Gln	Arg	Gly 160	Glu	Pro	Val	Ser	Cys 165	
ttc	ctc	ctg	cgt	atc	gaa	gac	aac	atg	gag	tcc	atc	gga	cgt	tcc	atc	643
Phe	Leu	Leu	Arg	Ile 170	Glu	Asp	Asn	Met	Glu	Ser	Ile	Gly	Arg	Ser	Ile 180	
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Asn	Ser	Ala	Leu 185	Gln	Leu	Ser	Lys	Arg 190	Gly	Gly	Gly	Val	Ala	Leu	Leu 195	
ctg	tcc	aac	ctt	cgt	gaa	gcc	ggg	gca	ccg	att	aag	aag	att	gaa	aac	739
Leu	Ser	Asn 200	Leu	Arg	Glu	Ala	Gly 205	Ala	Pro	Ile	Lys	Lys	Ile	Glu	Asn 210	
cag	tct	tcc	ggg	gtt	atc	cca	gtg	atg	aaa	ctt	ctg	gaa	gat	gct	ttc	787
Gln	Ser	Ser	Gly	Val	Ile 220	Pro	Val	Met	Lys	Leu	Leu	Glu	Asp	Ala	Phe 225	
tcc	tac	gct	aac	cag	ctg	ggg	gct	cgt	cag	ggg	gca	ggg	gct	gtg	tac	835
Ser	Tyr	Ala	Asn	Gln	Leu 235	Gly	Ala	Arg	Gln	Gly	Ala	Gly	Ala	Val	Tyr 245	
ctc	aac	gct	cac	cac	cca	gat	atc	ctg	tcc	ttc	ctg	gat	acc	aag	cgt	883
Leu	Asn	Ala	His	His 250	Pro	Asp	Ile	Leu	Ser	Phe	Leu	Asp	Thr	Lys	Arg 260	
gag	aac	gcc	gat	gag	aag	atc	cgc	atc	aag	acc	ctg	tcc	ctg	ggg	gtt	931
Glu	Asn	Ala	Asp 265	Glu	Lys	Ile	Arg	Ile 270	Lys	Thr	Leu	Ser	Leu	Gly	Val 275	
gtg	att	ccg	gac	atc	acc	ttc	gag	ctg	gct	aag	cgc	aac	gat	gac	atg	979
Val	Ile	Pro	Asp	Ile	Thr 280	Phe	Glu	Leu	Ala	Lys	Arg	Asn	Asp	Asp	Met 290	
tac	ctg	ttc	tcc	cca	tac	gat	gtg	gag	cgc	att	tac	ggc	aag	cct	ttc	1027
Tyr	Leu	Phe	Ser	Pro	Tyr 300	Asp	Val	Glu	Arg	Ile	Tyr 305	Gly	Lys	Pro	Phe	
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Ala	Asp	Val	Ser	Ile	Thr 315	Glu	His	Tyr	Asp	Glu	Met	Val	Asp	Asp	Asp 325	
cgc	atc	cgc	aag	acc	aag	atc	aac	gcg	cgt	cag	ttc	ttc	cag	acc	ctg	1123
Arg	Ile	Arg	Lys	Thr 330	Lys	Ile	Asn	Ala	Arg 335	Gln	Phe	Phe	Gln	Thr	Leu 340	
gca	gaa	atc	cag	ttc	gag	tcc	ggg	tac	cca	tac	atc	atg	tat	gaa	gac	1171
Ala	Glu	Ile	Gln	Phe 345	Glu	Ser	Gly	Tyr 350	Pro	Tyr	Ile	Met	Tyr	Glu	Asp 355	
acc	gtg	aat	gca	tcc	aac	cca	atc	gaa	ggg	cgc	atc	acc	cac	tca	aac	1219
Thr	Val	Asn	Ala	Ser	Asn 360	Pro	Ile	Glu	Gly	Arg	Ile	Thr	His	Ser	Asn 370	
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Leu	Cys	Ser	Glu	Ile	Leu 380	Gln	Val	Ser	Thr	Pro	Ser	Glu	Phe	Asn	Asp 385	
gac	ctg	act	tac	gca	gag	gtc	ggc	gaa	gac	att	tct	tgt	aac	ttg	ggg	1315
Asp	Leu	Thr	Tyr	Ala	Glu	Val	Gly	Glu	Asp	Ile	Ser	Cys	Asn	Leu	Gly	

390	395	400	405	
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Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro Asn Phe Glu Lys Thr	410	415	420	
atc gaa acc gaa atc cgc ggc tta act gca gtg cct gag cag acc agc				1411
Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val Pro Glu Gln Thr Ser	425	430	435	
atc gat tcc gtg cct tcc atc cgt aag ggc aac gaa gca gct cac gcc				1459
Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn Glu Ala Ala His Ala	440	445	450	
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Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr Phe Gly Arg Glu His	455	460	465	
atg cac tac ggc tcc gag gaa gcc ctg gac ttc acc aac gca tac ttt				1555
Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe Thr Asn Ala Tyr Phe	470	475	480	485
gct gcc gtg ctg tac cag tgc ctg cgt gca tcc aac cag atc gct act				1603
Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser Asn Gln Ile Ala Thr	490	495	500	
gag cgt gga gag cgt ttc aag aac ttc gaa aac tcc aag tat gca acc				1651
Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn Ser Lys Tyr Ala Thr	505	510	515	
ggt gag tac ttc gat gat ttc gat gca aac gac ttc gca cca aag tcc				1699
Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp Phe Ala Pro Lys Ser	520	525	530	
gac aag gtc aag gaa ctc ttt gcc aag tcg aac atc cac acc cca acc				1747
Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn Ile His Thr Pro Thr	535	540	545	
gtt gag gac tgg gct gcg ctg aag gcc gac gtg atg gag cac ggt ctg				1795
Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val Met Glu His Gly Leu	550	555	560	565
ttc aac cgt aac ctg caa gcg gtt cca cca acc ggt tcg atc tcc tac				1843
Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr Gly Ser Ile Ser Tyr	570	575	580	
atc aac aac tcc acc tcg tcg atc cac cca atc gca tcc aag att gag				1891
Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile Ala Ser Lys Ile Glu	585	590	595	
atc cgc aag gaa ggc aag atc ggc cgc gtt tac tac cca gct cca cac				1939
Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr Tyr Pro Ala Pro His	600	605	610	
atg gac aat gac aac ctt gag tac ttc gag gac gcc tac gaa atc ggc				1987
Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp Ala Tyr Glu Ile Gly	615	620	625	
tac gag aag atc att gac acc tac gct gtg gca acc aag tac gtt gac				2035
Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala Thr Lys Tyr Val Asp	630	635	640	645

cag ggc ctg tca ctg acc ttg ttc ttc aag gac act gcc acc acc cgt 2083
 Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp Thr Ala Thr Thr Arg
 650 655 660

gac atc aac cgt gcg cag atc tac gca tgg cgc aag ggc atc aag acc 2131
 Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg Lys Gly Ile Lys Thr
 665 670 675

ttg tac tac att cgc ctg cgc cag gtt gct ctg gaa ggc act gaa gtt 2179
 Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu Glu Gly Thr Glu Val
 680 685 690

gac ggc tgc gtc agc tgc atg ctg taaaagcact taaaaatata ccc 2226
 Asp Gly Cys Val Ser Cys Met Leu
 695 700

<210> 1066

<211> 701

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1066

Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn
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Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe
 20 25 30

Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu
 35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu
 50 55 60

Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr
 65 70 75 80

Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr
 85 90 95

Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg
 100 105 110

Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp
 115 120 125

Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe
 130 135 140

Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly
 145 150 155 160

Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser
 165 170 175

Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly
 180 185 190

Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile

195					200					205					
Lys	Lys	Ile	Glu	Asn	Gln	Ser	Ser	Gly	Val	Ile	Pro	Val	Met	Lys	Leu
210						215					220				
Leu	Glu	Asp	Ala	Phe	Ser	Tyr	Ala	Asn	Gln	Leu	Gly	Ala	Arg	Gln	Gly
225					230					235					240
Ala	Gly	Ala	Val	Tyr	Leu	Asn	Ala	His	His	Pro	Asp	Ile	Leu	Ser	Phe
				245					250					255	
Leu	Asp	Thr	Lys	Arg	Glu	Asn	Ala	Asp	Glu	Lys	Ile	Arg	Ile	Lys	Thr
			260					265					270		
Leu	Ser	Leu	Gly	Val	Val	Ile	Pro	Asp	Ile	Thr	Phe	Glu	Leu	Ala	Lys
		275					280					285			
Arg	Asn	Asp	Asp	Met	Tyr	Leu	Phe	Ser	Pro	Tyr	Asp	Val	Glu	Arg	Ile
	290					295					300				
Tyr	Gly	Lys	Pro	Phe	Ala	Asp	Val	Ser	Ile	Thr	Glu	His	Tyr	Asp	Glu
305					310					315					320
Met	Val	Asp	Asp	Asp	Arg	Ile	Arg	Lys	Thr	Lys	Ile	Asn	Ala	Arg	Gln
				325					330					335	
Phe	Phe	Gln	Thr	Leu	Ala	Glu	Ile	Gln	Phe	Glu	Ser	Gly	Tyr	Pro	Tyr
			340					345					350		
Ile	Met	Tyr	Glu	Asp	Thr	Val	Asn	Ala	Ser	Asn	Pro	Ile	Glu	Gly	Arg
		355					360					365			
Ile	Thr	His	Ser	Asn	Leu	Cys	Ser	Glu	Ile	Leu	Gln	Val	Ser	Thr	Pro
	370					375					380				
Ser	Glu	Phe	Asn	Asp	Asp	Leu	Thr	Tyr	Ala	Glu	Val	Gly	Glu	Asp	Ile
385					390					395					400
Ser	Cys	Asn	Leu	Gly	Ser	Leu	Asn	Val	Ala	Met	Ala	Met	Asp	Ala	Pro
			405						410					415	
Asn	Phe	Glu	Lys	Thr	Ile	Glu	Thr	Glu	Ile	Arg	Gly	Leu	Thr	Ala	Val
			420					425					430		
Pro	Glu	Gln	Thr	Ser	Ile	Asp	Ser	Val	Pro	Ser	Ile	Arg	Lys	Gly	Asn
		435					440					445			
Glu	Ala	Ala	His	Ala	Ile	Gly	Leu	Gly	Gln	Met	Asn	Leu	His	Gly	Tyr
	450					455					460				
Phe	Gly	Arg	Glu	His	Met	His	Tyr	Gly	Ser	Glu	Glu	Ala	Leu	Asp	Phe
465					470					475					480
Thr	Asn	Ala	Tyr	Phe	Ala	Ala	Val	Leu	Tyr	Gln	Cys	Leu	Arg	Ala	Ser
				485					490					495	
Asn	Gln	Ile	Ala	Thr	Glu	Arg	Gly	Glu	Arg	Phe	Lys	Asn	Phe	Glu	Asn
			500					505					510		
Ser	Lys	Tyr	Ala	Thr	Gly	Glu	Tyr	Phe	Asp	Asp	Phe	Asp	Ala	Asn	Asp
		515					520					525			

Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn
 530 535 540
 Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val
 545 550 555 560
 Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr
 565 570 575
 Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile
 580 585 590
 Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr
 595 600 605
 Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp
 610 615 620
 Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala
 625 630 635 640
 Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp
 645 650 655
 Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg
 660 665 670
 Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu
 675 680 685
 Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu
 690 695 700

<210> 1067

<211> 790

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(790)

<223> FRXA01079

<400> 1067

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gactgcatcg ggaaccaccg tcgtgccacg cggagaccag atg gac ttc cac gct 115
 Met Asp Phe His Ala
 1 5

ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163
 Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe
 10 15 20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211
 Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn
 25 30 35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259

Gln	Asn	Thr	Val	Phe	Phe	His	Asn	Leu	Gln	Glu	Lys	Ile	Asp	Tyr	Leu		
		40					45					50					
gtt	gaa	aac	aag	tac	tat	gac	cca	atc	gtt	ctg	gac	aag	tac	gac	ttc	307	
Val	Glu	Asn	Lys	Tyr	Tyr	Asp	Pro	Ile	Val	Leu	Asp	Lys	Tyr	Asp	Phe		
	55					60					65						
cag	ttc	atc	aag	gac	ctc	ttc	aag	cgc	gca	tac	gga	ttc	aag	ttc	cgc	355	
Gln	Phe	Ile	Lys	Asp	Leu	Phe	Lys	Arg	Ala	Tyr	Gly	Phe	Lys	Phe	Arg		
70					75				80						85		
ttc	cag	tcc	ttc	ctc	ggt	gca	tac	aag	tac	tac	act	tcc	tac	acc	ctg	403	
Phe	Gln	Ser	Phe	Leu	Gly	Ala	Tyr	Lys	Tyr	Tyr	Thr	Ser	Tyr	Thr	Leu		
				90					95					100			
aag	acc	ttc	gac	ggt	cgc	cgc	tac	ctc	gag	cgt	ttc	gaa	gac	cgt	gtc	451	
Lys	Thr	Phe	Asp	Gly	Arg	Arg	Tyr	Leu	Glu	Arg	Phe	Glu	Asp	Arg	Val		
			105					110					115				
tgc	atg	gtc	gcc	ctc	acc	ctc	gct	gac	ggc	gac	cgc	gca	ttg	gcc	gag	499	
Cys	Met	Val	Ala	Leu	Thr	Leu	Ala	Asp	Gly	Asp	Arg	Ala	Leu	Ala	Glu		
		120					125					130					
aac	ctg	gtc	gat	gag	atc	atg	tct	ggc	cgt	ttc	caa	cca	gca	acc	cca	547	
Asn	Leu	Val	Asp	Glu	Ile	Met	Ser	Gly	Arg	Phe	Gln	Pro	Ala	Thr	Pro		
	135					140					145						
acc	ttc	ctg	aac	tcc	ggc	aag	gca	cag	cgc	ggc	gag	cca	gta	tcc	tgc	595	
Thr	Phe	Leu	Asn	Ser	Gly	Lys	Ala	Gln	Arg	Gly	Glu	Pro	Val	Ser	Cys		
150					155				160						165		
ttc	ctc	ctg	cgt	atc	gaa	gac	aac	atg	gag	tcc	atc	gga	cgt	tcc	atc	643	
Phe	Leu	Leu	Arg	Ile	Glu	Asp	Asn	Met	Glu	Ser	Ile	Gly	Arg	Ser	Ile		
				170					175					180			
aac	tct	gct	ctt	cag	ctg	tcc	aag	cgt	ggc	ggt	ggc	gta	gcg	ttg	ctg	691	
Asn	Ser	Ala	Leu	Gln	Leu	Ser	Lys	Arg	Gly	Gly	Gly	Val	Ala	Leu	Leu		
			185					190					195				
ctg	tcc	aac	ctt	cgt	gaa	gcc	ggt	gca	cgc	att	aag	aag	att	gaa	atc	739	
Leu	Ser	Asn	Leu	Arg	Glu	Ala	Gly	Ala	Pro	Ile	Lys	Lys	Ile	Glu	Ile		
		200					205						210				
cag	tct	tcc	ggt	gtt	atc	cca	gtg	atg	aaa	ctt	ctg	gaa	gat	gct	ttc	787	
Gln	Ser	Ser	Gly	Val	Ile	Pro	Val	Met	Lys	Leu	Leu	Glu	Asp	Ala	Phe		
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tcc																790	
Ser																	
230																	

<210> 1068

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 1068

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 20 25 30
 Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu
 35 40 45
 Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu
 50 55 60
 Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr
 65 70 75 80
 Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr
 85 90 95
 Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg
 100 105 110
 Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp
 115 120 125
 Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe
 130 135 140
 Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly
 145 150 155 160
 Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser
 165 170 175
 Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly
 180 185 190
 Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile
 195 200 205
 Lys Lys Ile Glu Ile Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu
 210 215 220
 Leu Glu Asp Ala Phe Ser
 225 230

<210> 1069

<211> 1364

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1341)

<223> FRXA01084

<400> 1069

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 1 5 10 15

aag acc ctg tcc ctg ggt gtt gtg att ccg gac atc acc ttc gag ctg 96
 Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu
 20 25 30

gct aag cgc aac gat gac atg tac ctg ttc tcc cca tac gat gtg gag	144
Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu	
35 40 45	
cgc att tac ggc aag cct ttc gca gac gtc tca atc acc gag cac tac	192
Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr	
50 55 60	
gac gag atg gtg gat gat gac cgc atc cgc aag acc aag atc aac gcg	240
Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala	
65 70 75 80	
cgt cag ttc ttc cag acc ctg gca gaa atc cag ttc gag tcc ggt tac	288
Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr	
85 90 95	
cca tac atc atg tat gaa gac acc gtg aat gca tcc aac cca atc gaa	336
Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu	
100 105 110	
ggc cgc atc acc cac tca aac ctg tgc tct gag atc ctt cag gtg tcc	384
Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser	
115 120 125	
acc cca tct gaa ttc aac gat gac ctg act tac gca gag gtc ggc gaa	432
Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu	
130 135 140	
gac att tct tgt aac ttg ggt tcc ctc aac gtt gca atg gct atg gat	480
Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp	
145 150 155 160	
gca cca aac ttt gag aag acc atn gaa acc gaa atc cgc ggc tta act	528
Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr	
165 170 175	
gca gtg nct gag cag acc agc atc gat tcc gtg cct tcc atc cgt aag	576
Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys	
180 185 190	
ggc aac gaa gca gct cac gcc atc ggc ctt ggc cag atg aac ctt cac	624
Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His	
195 200 205	
ggc tac ttc ggt cgc gag cac atg cac tac ggc tcc gag gaa gcc ctg	672
Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu	
210 215 220	
gac ttc acc aac gca tac ttt gct gcc gtg ctg tac cag tgc ctg cgt	720
Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg	
225 230 235 240	
gca tcc aac cag atc gct act gag cgt gga gag cgt ttc aag aac ttc	768
Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe	
245 250 255	
gaa aac tcc aag tat gca acc ggt gag tac ttc gat gat ttc gat gca	816
Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala	
260 265 270	

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aac gac ttc gca cca aag tcc gac aag gtc aag gaa ctc ttt gcc aag      864
Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys
      275                      280                      285

tcg aac atc cac acc cca acc gtt gag gac tgg gct gcg ctg aag gcc      912
Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala
      290                      295                      300

gac gtg atg gag cac ggt ctg ttc aac cgt aac ctg caa gcg gtt cca      960
Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro
      305                      310                      315                      320

cca acc ggt tcg atc tcc tac atc aac aac tcc acc tcg tcg atc cac      1008
Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His
      325                      330                      335

cca atc gca tcc aag att gag atc cgc aag gaa ggc aag atc ggc cgc      1056
Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg
      340                      345                      350

gtt tac tac cca gct cca cac atg gac aat gac aac ctt gag tac ttc      1104
Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe
      355                      360                      365

gag gac gcc tac gaa atc ggc tac gag aag atc att gac acc tac gct      1152
Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala
      370                      375                      380

gtg gca acc aag tac gtt gac cag ggc ctg tca ctg acc ttg ttc ttc      1200
Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe
      385                      390                      395                      400

aag gac act gcc acc acc cgt gac atc aac cgt gcg cag atc tac gca      1248
Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala
      405                      410                      415

tgg cgc aag ggc atc aag acc ttg tac tac att cgc ctg cgc cag gtt      1296
Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val
      420                      425                      430

gct ctg gaa ggc act gaa gtt gac ggc tgc gtc agc tgc atg ctg      1341
Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu
      435                      440                      445

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<210> 1070

<211> 447

<212> PRT

<213> Corynebacterium glutamicum

<400> 1070

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Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile
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Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu
  20                      25                      30

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Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu
  35                      40                      45

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Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr
 50 55 60
 Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala
 65 70 75 80
 Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr
 85 90 95
 Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu
 100 105 110
 Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser
 115 120 125
 Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu
 130 135 140
 Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp
 145 150 155 160
 Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr
 165 170 175
 Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys
 180 185 190
 Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His
 195 200 205
 Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu
 210 215 220
 Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg
 225 230 235 240
 Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe
 245 250 255
 Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala
 260 265 270
 Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys
 275 280 285
 Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala
 290 295 300
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro
 305 310 315 320
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His
 325 330 335
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg
 340 345 350
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe
 355 360 365

Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala
 370 375 380
 Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe
 385 390 395 400
 Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala
 405 410 415
 Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val
 420 425 430
 Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu
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<210> 1071

<211> 1125

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1102)

<223> RXN01920

<400> 1071

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 Met Ala Ala Asp Ser
 1 5

 gat ctc agt gtt cac gat gct tac tta aag gag cat gtt gca cct gta 163
 Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu His Val Ala Pro Val
 10 15 20

 aag gcg atc aac tgg aac tcc atc cca gat tcc aaa gat ctt gaa gtc 211
 Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser Lys Asp Leu Glu Val
 25 30 35

 tgg gat cgt ctg acc ggt aac ttc tgg ctc cca gaa aag gtc cca gta 259
 Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro Glu Lys Val Pro Val
 40 45 50

 tcc aac gac atc aag agc tgg gga acc ctc aac gag gtt gaa aaa gcc 307
 Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn Glu Val Glu Lys Ala
 55 60 65

 gca acc atg cgc gtg ttc acc gga ctt acc ctg ctg gac acc att cag 355
 Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu Leu Asp Thr Ile Gln
 70 75 80 85

 ggc act gtc ggc gca atc tcc ctg ctt cca gac gca gat tca ctg cac 403
 Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp Ala Asp Ser Leu His
 90 95 100

 gaa gaa gcg gtg cta acc aac att gcg ttc atg gaa tcc gtg cac gca 451
 Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met Glu Ser Val His Ala
 105 110 115

aag agt tac tcc aac atc ttc atg act ctg gcc tcc acc gcg gaa atc 499
Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala Ser Thr Ala Glu Ile
120 125 130

aac gat gcg ttc cgt tgg tct gag gaa aat gaa aac ctg cag cgc aag 547
Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu Asn Leu Gln Arg Lys
135 140 145

gca aag atc atc ctg tct tac tat gag ggc gat gat cca cta aag cgc 595
Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp Asp Pro Leu Lys Arg
150 155 160 165

aag atc gcc tcc gtg atc ctg gag tcc ttc ctg ttc tac tcc ggc ttc 643
Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu Phe Tyr Ser Gly Phe
170 175 180

tac ctc cca atg tat tgg tcc agc cac tcc aag ctg gcc aac acc gcc 691
Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys Leu Ala Asn Thr Ala
185 190 195

gac gtg atc cgc ctg atc atc cgc gat gag gca gtg cac ggc tac tac 739
Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr Tyr
200 205 210

att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag cgt 787
Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu Arg
215 220 225

cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt tac 835
Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu Tyr
230 235 240 245

gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga tgg 883
Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly Trp
250 255 260

acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc ctc 931
Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala Leu
265 270 275

aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag gtg 979
Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys Val
280 285 290

tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac cac 1027
Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn His
295 300 305

gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca gaa 1075
Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala Glu
310 315 320 325

aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag 1122
Asn Thr Glu Asp Asp Asp Trp Asp Phe
330

cgc 1125

<210> 1072

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 1072

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His	Val	Ala	Pro	Val	Lys	Ala	Ile	Asn	Trp	Asn	Ser	Ile	Pro	Asp	Ser	20	25	30	
Lys	Asp	Leu	Glu	Val	Trp	Asp	Arg	Leu	Thr	Gly	Asn	Phe	Trp	Leu	Pro	35	40	45	
Glu	Lys	Val	Pro	Val	Ser	Asn	Asp	Ile	Lys	Ser	Trp	Gly	Thr	Leu	Asn	50	55	60	
Glu	Val	Glu	Lys	Ala	Ala	Thr	Met	Arg	Val	Phe	Thr	Gly	Leu	Thr	Leu	65	70	75	80
Leu	Asp	Thr	Ile	Gln	Gly	Thr	Val	Gly	Ala	Ile	Ser	Leu	Leu	Pro	Asp	85	90	95	
Ala	Asp	Ser	Leu	His	Glu	Glu	Ala	Val	Leu	Thr	Asn	Ile	Ala	Phe	Met	100	105	110	
Glu	Ser	Val	His	Ala	Lys	Ser	Tyr	Ser	Asn	Ile	Phe	Met	Thr	Leu	Ala	115	120	125	
Ser	Thr	Ala	Glu	Ile	Asn	Asp	Ala	Phe	Arg	Trp	Ser	Glu	Glu	Asn	Glu	130	135	140	
Asn	Leu	Gln	Arg	Lys	Ala	Lys	Ile	Ile	Leu	Ser	Tyr	Tyr	Glu	Gly	Asp	145	150	155	160
Asp	Pro	Leu	Lys	Arg	Lys	Ile	Ala	Ser	Val	Ile	Leu	Glu	Ser	Phe	Leu	165	170	175	
Phe	Tyr	Ser	Gly	Phe	Tyr	Leu	Pro	Met	Tyr	Trp	Ser	Ser	His	Ser	Lys	180	185	190	
Leu	Ala	Asn	Thr	Ala	Asp	Val	Ile	Arg	Leu	Ile	Ile	Arg	Asp	Glu	Ala	195	200	205	
Val	His	Gly	Tyr	Tyr	Ile	Gly	Tyr	Lys	Tyr	Gln	Lys	Ala	Val	Ala	Lys	210	215	220	
Glu	Thr	Pro	Glu	Arg	Gln	Glu	Glu	Leu	Lys	Glu	Tyr	Thr	Phe	Asp	Leu	225	230	235	240
Leu	Tyr	Asp	Leu	Tyr	Asp	Asn	Glu	Thr	Gln	Tyr	Ser	Glu	Asp	Leu	Tyr	245	250	255	
Asp	Asp	Leu	Gly	Trp	Thr	Glu	Asp	Val	Lys	Arg	Phe	Leu	Arg	Tyr	Asn	260	265	270	
Ala	Asn	Lys	Ala	Leu	Asn	Asn	Leu	Gly	Tyr	Glu	Gly	Leu	Phe	Pro	Ala	275	280	285	
Asp	Glu	Thr	Lys	Val	Ser	Pro	Asn	Ile	Leu	Ser	Ala	Leu	Ser	Pro	Asn	290	295	300	

Ala Asp Glu Asn His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val
 305 310 315 320

Ile Gly Lys Ala Glu Asn Thr Glu Asp Asp Trp Asp Phe
 325 330

<210> 1073

<211> 437

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(414)

<223> FRXA01920

<400> 1073

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Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr	
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tac att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag	96
Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu	
20 25 30	
cgt cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt	144
Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu	
35 40 45	
tac gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga	192
Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly	
50 55 60	
tgg acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc	240
Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala	
65 70 75 80	
ctc aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag	288
Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys	
85 90 95	
gtg tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac	336
Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn	
100 105 110	
cac gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca	384
His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala	
115 120 125	
gaa aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag	434
Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe	
130 135	
cgc	437

<210> 1074

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 1074

Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr
 1 5 10 15

Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu
 20 25 30

Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu
 35 40 45

Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly
 50 55 60

Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala
 65 70 75 80

Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys
 85 90 95

Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn
 100 105 110

His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala
 115 120 125

Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
 130 135

<210> 1075

<211> 567

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(544)

<223> RXA01080

<400> 1075

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ttgcgcacaa acggtattta gaagggaagt gagttcgagg atg cta atc gtg tat 115
 Met Leu Ile Val Tyr
 1 5

ttt tcc tcg gcc acc gac aac acg cat cgt ttt gta caa aag ctc gat 163
 Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe Val Gln Lys Leu Asp
 10 15 20

tta ccc aac gtg cgc atc ccc ctc act agg gtg gaa gaa ccg ctg aaa 211
 Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val Glu Glu Pro Leu Lys
 25 30 35

atc aac gag ccc tac gtg cta atc acc ccg acc tat ggt ggt gga gtc 259
 Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr Tyr Gly Gly Gly Val
 40 45 50

tcc atg act gga gaa aac tcc cgc ccg gtc cca cca caa gtc atc agg 307
 Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro Pro Gln Val Ile Arg

55 60 65
 ttt tta aat gat gaa cac aac cgc agc ttc atc agg gca gtt gtt gca 355
 Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile Arg Ala Val Val Ala
 70 75 80 85
 ggt gga aac tca aac ttc ggc tcc gat ttt ggg ttg gca ggc gag atc 403
 Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly Leu Ala Gly Glu Ile
 90 95 100
 att tcc aag aaa tgt aaa gtg ccc tat gtc tac cgt ttc gag ctc atg 451
 Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr Arg Phe Glu Leu Met
 105 110 115
 ggc aat gag gaa gat gta agt atc ctt cgt gga ggt ctt act caa aac 499
 Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly Gly Leu Thr Gln Asn
 120 125 130
 gcc caa gct ttg ggg ctg gaa cca caa gaa cca gtt acc tcg cga 544
 Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro Val Thr Ser Arg
 135 140 145
 taaaccttaa aacttaatca atc 567

 <210> 1076
 <211> 148
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1076
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 1 5 10 15
 Val Gln Lys Leu Asp Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val
 20 25 30
 Glu Glu Pro Leu Lys Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr
 35 40 45
 Tyr Gly Gly Gly Val Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro
 50 55 60
 Pro Gln Val Ile Arg Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile
 65 70 75 80
 Arg Ala Val Val Ala Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly
 85 90 95
 Leu Ala Gly Glu Ile Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr
 100 105 110
 Arg Phe Glu Leu Met Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly
 115 120 125
 Gly Leu Thr Gln Asn Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro
 130 135 140
 Val Thr Ser Arg
 145

<210> 1077
 <211> 650
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(627)
 <223> RXA00867

<400> 1077
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 Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr
 1 5 10 15
 gca ctt cag ctg gac acc aag ctg gac ggc att cct tcc aag gtg ctc 96
 Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu
 20 25 30
 tcc gat gcg ctt gag cag gca cgc gat gcc cga ctg acc atc ctg aac 144
 Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn
 35 40 45
 acc atg gct gat gtc atc aac gga cct gat gag atg agc aag ttc gct 192
 Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala
 50 55 60
 cct cgc atc acc acc gtg aag atc cca gtg gca aag atc ggt gag ctg 240
 Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu
 65 70 75 80
 atc gga cca aag ggt aag aac atc aac gct ctt acc gaa gag acc ggc 288
 Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly
 85 90 95
 gca aac atc tcc atc gaa gat gac ggc acc gtg ttc atc tct gca gct 336
 Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala
 100 105 110
 gac ggc gca tct gct gaa gcg gcg atc gaa aag atc aac gct ctg gcg 384
 Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala
 115 120 125
 aac cca cag ctg cca aag gtt ggc gag cgc ttc ctc gga acc gtc gtc 432
 Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val
 130 135 140
 aag acc acc gca ttc gga gca ttc gtt tcc ttg ctc cca ggc cgc gac 480
 Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp
 145 150 155 160
 ggc ctt gtt cac atc tcc aag ctg ggt aac ggc aag cga gta gaa aag 528
 Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys
 165 170 175
 gtc gac gat gtg gtg aag gtt ggc gag aag att cag gtc gaa atc gct 576
 Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala
 180 185 190
 gac atc gac aac cgc ggc aag atc tcc ttg gtc cca gtt gtt gaa gag 624

Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu
 195 200 205

gac taattagttc tggctagatc ggg
 Asp

650

<210> 1078

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 1078

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Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu
 20 25 30

Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn
 35 40 45

Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala
 50 55 60

Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu
 65 70 75 80

Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly
 85 90 95

Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala
 100 105 110

Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala
 115 120 125

Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val
 130 135 140

Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp
 145 150 155 160

Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys
 165 170 175

Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala
 180 185 190

Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu
 195 200 205

Asp

<210> 1079

<211> 630

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(630)

<223> RXA01416

<400> 1079

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gca cca acc gaa aag atc gtc tcc gac ggc ctt gaa gca gct aag cca	96
Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro	
20 25 30	
ttc atc gac atc ctg tgc cgc gca cag gaa ggt ctg gca cag cgc gtt	144
Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val	
35 40 45	
gga aac gca gcc aag gaa ttc cca ctg ttc cct cca tac acc gac gag	192
Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu	
50 55 60	
gtg tac tcc gca gtg gag cgc aag gta tcc aag aag cta gct tct ttg	240
Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu	
65 70 75 80	
ctg acc ctg aag gca aag caa gag cgc gac gac gct acc aac gcc tac	288
Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Ala Thr Asn Ala Tyr	
85 90 95	
atg gaa gaa atc gaa gcc gaa ctg ctt cca aag ttc gag gct tcc tac	336
Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr	
100 105 110	
agc tca gca gct gaa gcg tcc aag gaa atc cgt gca gga tac aac gct	384
Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala	
115 120 125	
gtc atg aag gcc atc gtg cgc cgc atg atc ctc acc gat cac ttc cgc	432
Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg	
130 135 140	
atc gac ggc cgc gga gtc acc gac atc cgt gac ctg gca gta gaa gtt	480
Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val	
145 150 155 160	
gag ctc atc cca cgt gcg cac ggt tcc tcc ctc ttc gag cgt ggc gag	528
Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu	
165 170 175	
acc cag atc ctt ggt gtc acc acc ctg gac atg ctc aag atg gaa cag	576
Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln	
180 185 190	
caa atc gac tcc ctg gca cca ggc gat gcg aag cgc tac atg cac cac	624
Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His	
195 200 205	
tac aac	630
Tyr Asn	

210

<210> 1080

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 1080

Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro
 1 5 10 15

Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro
 20 25 30

Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val
 35 40 45

Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu
 50 55 60

Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu
 65 70 75 80

Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr
 85 90 95

Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr
 100 105 110

Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala
 115 120 125

Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg
 130 135 140

Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val
 145 150 155 160

Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu
 165 170 175

Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln
 180 185 190

Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His
 195 200 205

Tyr Asn
 210

<210> 1081

<211> 757

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> RXA01486

<400> 1081

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atcgccgagc agaactaaac atgaggagac ctactcgcac atg agc gat gta aag 115
                               Met Ser Asp Val Lys
                               1 5

gac ttc gaa gac acc gaa ttt ggc ctg atc gag gcc gtc gca acc atc 163
Asp Phe Glu Asp Thr Glu Phe Gly Leu Ile Glu Ala Val Ala Thr Ile
                        10 15 20

gac aac ggt gac ttc gga acc cgc acc atc cgt ttt gaa acc ggc caa 211
Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg Phe Glu Thr Gly Gln
                        25 30 35

ctt gcc cgc cag gca gat ggt gca gtg acc acc tac ctc gac gat gac 259
Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr Tyr Leu Asp Asp Asp
                        40 45 50

acg atg ctg ctg gca acc acc acc gca tcc aac cag cca cgc gag ggc 307
Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn Gln Pro Arg Glu Gly
                        55 60 65

ttt gac ttc ttc cca ctg acc gtg gac gtt gaa gag cgt atg tac gca 355
Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu Glu Arg Met Tyr Ala
                        70 75 80 85

gct ggt cgc atc cct ggc tct ttc ttc cgt cgg gag ggt cgc cca tcc 403
Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg Glu Gly Arg Pro Ser
                        90 95 100

acc gaa gct atc ctg gct tgc cgt ctc atc gac cgc cca ctg cgc cca 451
Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp Arg Pro Leu Arg Pro
                        105 110 115

acc ttt gtt aag ggc ctg cgc aat gag gtt cag atc gtt gtc acc gtc 499
Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln Ile Val Val Thr Val
                        120 125 130

atg tcc atg aac cct gag gat tac tac gat gtc gta gca atc aac gga 547
Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val Val Ala Ile Asn Gly
                        135 140 145

gct tcc gca gca acc cgc atc tcc gga ctt cct gtc tcc ggc gct gtc 595
Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro Val Ser Gly Ala Val
                        150 155 160 165

ggt ggc gtt cgc atg gca ctg gtt ggt gat gaa aag cac cca gaa ggc 643
Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu Lys His Pro Glu Gly
                        170 175 180

caa tgg gtt gca ttc cca acc cac gct caa cat gag cag tcc gta ttt 691
Gln Trp Val Ala Phe Pro Thr His Ala Gln His Glu Gln Ser Val Phe
                        185 190 195

gaa atc gtt gtg gct ggt cgc ctc gtc gag cgc aag cgc ggc aac aag 739
Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg Lys Arg Gly Asn Lys
                        200 205 210

acc ttc tcc gac gtc gca 757

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Thr Phe Ser Asp Val Ala
215

<210> 1082

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1082

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20 25 30

Phe Glu Thr Gly Gln Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr
35 40 45

Tyr Leu Asp Asp Asp Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn
50 55 60

Gln Pro Arg Glu Gly Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu
65 70 75 80

Glu Arg Met Tyr Ala Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg
85 90 95

Glu Gly Arg Pro Ser Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp
100 105 110

Arg Pro Leu Arg Pro Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln
115 120 125

Ile Val Val Thr Val Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val
130 135 140

Val Ala Ile Asn Gly Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro
145 150 155 160

Val Ser Gly Ala Val Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu
165 170 175

Lys His Pro Glu Gly Gln Trp Val Ala Phe Pro Thr His Ala Gln His
180 185 190

Glu Gln Ser Val Phe Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg
195 200 205

Lys Arg Gly Asn Lys Thr Phe Ser Asp Val Ala
210 215

<210> 1083

<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01678

<400> 1083

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cggtctatata tctgcaactg cagctcaccc cggtgcagca atg ctg aaa tgt gca 115
Met Leu Lys Cys Ala
1 5

gtc gat gaa gcc gct ggc gga cgc gcc caa gct ttc gta tcc tca ggc 163
Val Asp Glu Ala Ala Gly Gly Arg Ala Gln Ala Phe Val Ser Ser Gly
10 15 20

gat aac att ggt ggc agc ccg ttc caa tcc tcc att ctt ggt gat gaa 211
Asp Asn Ile Gly Gly Ser Pro Phe Gln Ser Ser Ile Leu Gly Asp Glu
25 30 35

ccc acc ttg gaa gca ctc aac caa atg ggt ctt gat tac tca gca gtg 259
Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu Asp Tyr Ser Ala Val
40 45 50

ggc aac cac gaa ttt gat aaa ggc tac gca gac tta agc agt cga gtc 307
Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp Leu Ser Ser Arg Val
55 60 65

gct gac ctt gct gat ttt gat tat ctc ggc gca aac gtt gag ggc gaa 355
Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala Asn Val Glu Gly Glu
70 75 80 85

aac cca gat ctt gca cca tat gga att tct cac ctt gat ggt gtg aag 403
Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His Leu Asp Gly Val Lys
90 95 100

gtt gct ttc gta ggc acc gta tcc caa gaa act ccg atg ttg gtc aat 451
Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr Pro Met Leu Val Asn
105 110 115

tct gaa ggc att gag gga atc acg ttt act gac cca ctt gaa gca acc 499
Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp Pro Leu Glu Ala Thr
120 125 130

aac cgt gta gct gat gaa ctc gtg gga agt ggc gca gca gat gtt gtc 547
Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly Ala Ala Asp Val Val
135 140 145

gtt gcg ctt tac cac gaa ggc att acc ggc acc gaa gca tgg tca gaa 595
Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr Glu Ala Trp Ser Glu
150 155 160 165

aat atc gac gtt gtt ttc gca ggt cac acc cac taagtctgtg atctaggaac 648
Asn Ile Asp Val Val Phe Ala Gly His Thr His
170 175

cga 651

<210> 1084

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 1084

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          20          25          30

Ile Leu Gly Asp Glu Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu
          35          40          45

Asp Tyr Ser Ala Val Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp
          50          55          60

Leu Ser Ser Arg Val Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala
          65          70          75          80

Asn Val Glu Gly Glu Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His
          85          90          95

Leu Asp Gly Val Lys Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr
          100          105          110

Pro Met Leu Val Asn Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp
          115          120          125

Pro Leu Glu Ala Thr Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly
          130          135          140

Ala Ala Asp Val Val Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr
          145          150          155          160

Glu Ala Trp Ser Glu Asn Ile Asp Val Val Phe Ala Gly His Thr His
          165          170          175

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<210> 1085

<211> 1359

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1336)

<223> RXA01679

<400> 1085

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                                     Met Gln Ser Gly Asn
                                     1          5

tac ggg cac gca ctt gcc gat gta gat ttc agc ttc aac cac gac acc 163
Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser Phe Asn His Asp Thr
          10          15          20

ggg gag ctc acc gta gat gat gcc cgc atg ctc gga gtc gac gat atc 211
Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu Gly Val Asp Asp Ile

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25						30						35						
aac	gcg	tgt	gaa	aac	cca	gat	gac	acc	att	gca	gat	att	gtt	gct	cag	259		
Asn	Ala	Cys	Glu	Asn	Pro	Asp	Asp	Thr	Ile	Ala	Asp	Ile	Val	Ala	Gln			
	40						45					50						
gcg	gaa	ctt	gat	gct	ggc	gaa	gcc	ggc	aaa	gaa	gta	gta	gcg	acc	atc	307		
Ala	Glu	Leu	Asp	Ala	Gly	Glu	Ala	Gly	Lys	Glu	Val	Val	Ala	Thr	Ile			
	55					60					65							
gat	ggc	gat	ttt	ctc	cgc	gcc	agc	gac	gaa	gga	gca	gaa	tct	ggc	tcc	355		
Asp	Gly	Asp	Phe	Leu	Arg	Ala	Ser	Asp	Glu	Gly	Ala	Glu	Ser	Gly	Ser			
	70				75					80					85			
aac	tac	ggc	gct	gaa	tcc	cag	ctc	gtc	aac	atg	att	gcc	agt	gct	gtg	403		
Asn	Tyr	Gly	Ala	Glu	Ser	Gln	Leu	Val	Asn	Met	Ile	Ala	Ser	Ala	Val			
				90					95					100				
cgt	tgg	tcc	atg	tcc	acc	aat	acc	gcc	acc	acc	gca	gac	att	ggg	ctt	451		
Arg	Trp	Ser	Met	Ser	Thr	Asn	Thr	Ala	Thr	Thr	Ala	Asp	Ile	Gly	Leu			
			105					110					115					
atg	aac	gcc	gga	gga	ctc	cac	act	gac	cta	ttc	agc	ggc	gat	gtt	acc	499		
Met	Asn	Ala	Gly	Gly	Leu	His	Thr	Asp	Leu	Phe	Ser	Gly	Asp	Val	Thr			
		120					125					130						
tac	gcc	gaa	gct	ttt	gaa	atc	cag	cct	ttc	tcc	ggc	gaa	gat	tca	ttt	547		
Tyr	Ala	Glu	Ala	Phe	Glu	Ile	Gln	Pro	Phe	Ser	Gly	Glu	Asp	Ser	Phe			
	135					140					145							
gtc	acc	ctc	aag	gga	tca	gtc	ttc	aaa	gat	gcc	ctt	gac	cag	cag	tgg	595		
Val	Thr	Leu	Lys	Gly	Ser	Val	Phe	Lys	Asp	Ala	Leu	Asp	Gln	Gln	Trp			
	150				155					160					165			
gaa	gaa	ggc	tct	gca	cga	cca	gtg	gca	gca	ctt	ggc	gta	tcc	gac	aac	643		
Glu	Glu	Gly	Ser	Ala	Arg	Pro	Val	Ala	Ala	Leu	Gly	Val	Ser	Asp	Asn			
				170				175						180				
gtt	tcc	tac	acc	tac	gac	atc	aac	cgt	cca	atc	ggc	gac	cgc	gtc	act	691		
Val	Ser	Tyr	Thr	Tyr	Asp	Ile	Asn	Arg	Pro	Ile	Gly	Asp	Arg	Val	Thr			
			185				190						195					
tcc	gtg	acc	att	gat	gat	acc	cca	ctt	gat	ccg	gaa	cgc	gac	tac	gtt	739		
Ser	Val	Thr	Ile	Asp	Asp	Thr	Pro	Leu	Asp	Pro	Glu	Arg	Asp	Tyr	Val			
		200					205					210						
gtt	gca	gct	tcc	ctg	tac	ctc	cag	tcc	ggc	aac	gaa	ggc	atg	acc	gca	787		
Val	Ala	Ala	Ser	Leu	Tyr	Leu	Gln	Ser	Gly	Asn	Glu	Gly	Met	Thr	Ala			
	215					220					225							
ctg	acc	cgc	gga	acc	gca	cct	gca	caa	acc	ggc	atc	gtg	gat	gta	cag	835		
Leu	Thr	Arg	Gly	Thr	Ala	Pro	Ala	Gln	Thr	Gly	Ile	Val	Asp	Val	Gln			
	230				235					240					245			
tcc	acc	atc	gga	tac	ttg	tcc	aac	aac	aat	gtc	acc	cca	cgt	act	ggc	883		
Ser	Thr	Ile	Gly	Tyr	Leu	Ser	Asn	Asn	Asn	Val	Thr	Pro	Arg	Thr	Gly			
				250				255						260				
caa	gcc	cag	att	tcc	atc	acc	cca	tcc	ggc	gag	ttc	aat	gcg	ggc	gaa	931		
Gln	Ala	Gln	Ile	Ser	Ile	Thr	Pro	Ser	Gly	Glu	Phe	Asn	Ala	Gly	Glu			
			265					270					275					

acc atc acc ctt gac atg gca gga ctc cgc tac acc caa ggc gac act 979
 Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr Thr Gln Gly Asp Thr
 280 285 290

gcc acg gaa gta act gtc agc ctt cga gaa gaa att gtt tca gca cca 1027
 Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu Ile Val Ser Ala Pro
 295 300 305

att gat cct cag ctc gga gaa gct ggc ttt ggc gaa gct gga acc gcg 1075
 Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly Glu Ala Gly Thr Ala
 310 315 320 325

aca gtg agc ttg gac att cct gca acc ctt tca ggt act caa aac ctc 1123
 Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser Gly Thr Gln Asn Leu
 330 335 340

gtt gtc acc acc gat acc ggc acc cgt att tcc atg cca gtt gag att 1171
 Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser Met Pro Val Glu Ile
 345 350 355

gtt ggc gca gaa caa cca gca ccg caa cca gca ggt tcc tct gtt tta 1219
 Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala Gly Ser Ser Val Leu
 360 365 370

gga act gga gtg ctc agt gga ctc ctc ggc att gtt gta gga att cta 1267
 Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile Val Val Gly Ile Leu
 375 380 385

gga atg gtc ggt ctg gtg aac tgg att gac cca agc ttc att caa cag 1315
 Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro Ser Phe Ile Gln Gln
 390 395 400 405

atc cag cag caa atc ttt gct taaatttagt aaaaagcatg cat 1359
 Ile Gln Gln Gln Ile Phe Ala
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<210> 1086

<211> 412

<212> PRT

<213> Corynebacterium glutamicum

<400> 1086

Met Gln Ser Gly Asn Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser
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Phe Asn His Asp Thr Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu
 20 25 30

Gly Val Asp Asp Ile Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala
 35 40 45

Asp Ile Val Ala Gln Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu
 50 55 60

Val Val Ala Thr Ile Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly
 65 70 75 80

Ala Glu Ser Gly Ser Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met
 85 90 95

Ile Ala Ser Ala Val Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr
 100 105 110
 Ala Asp Ile Gly Leu Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe
 115 120 125
 Ser Gly Asp Val Thr Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser
 130 135 140
 Gly Glu Asp Ser Phe Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala
 145 150 155 160
 Leu Asp Gln Gln Trp Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu
 165 170 175
 Gly Val Ser Asp Asn Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile
 180 185 190
 Gly Asp Arg Val Thr Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro
 195 200 205
 Glu Arg Asp Tyr Val Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn
 210 215 220
 Glu Gly Met Thr Ala Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly
 225 230 235 240
 Ile Val Asp Val Gln Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val
 245 250 255
 Thr Pro Arg Thr Gly Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu
 260 265 270
 Phe Asn Ala Gly Glu Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr
 275 280 285
 Thr Gln Gly Asp Thr Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu
 290 295 300
 Ile Val Ser Ala Pro Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly
 305 310 315 320
 Glu Ala Gly Thr Ala Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser
 325 330 335
 Gly Thr Gln Asn Leu Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser
 340 345 350
 Met Pro Val Glu Ile Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala
 355 360 365
 Gly Ser Ser Val Leu Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile
 370 375 380
 Val Val Gly Ile Leu Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro
 385 390 395 400
 Ser Phe Ile Gln Gln Ile Gln Gln Gln Ile Phe Ala
 405 410


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<220>
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<222> (101) .. (1048)
<223> RXN01488
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<400> 1087																
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gcccgcacctt aaaaataaaaa acctgaaagg ttaaaaacgc atg agc aaa aaa gcc																115
Met Ser Lys Lys Ala																5
atc ctt gat atc gac acc ggc atc gat gat gcc ctc gca ctt gcc tac																163
Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ala Tyr																20
gca ctg ggc tca cct gaa cta gag ctc att ggt gtc acc acc acc tac																211
Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly Val Thr Thr Thr Tyr																35
ggt aac gtg cta ctc gaa acc ggt gca gtc aat gac ctg gca ctg ctt																259
Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu																50
gat ctg ttc ggt gca cca gaa gta cct gtg tac ttg ggt gag cca cac																307
Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His																65
gca cag acc aag gat ggc ttt gaa gtt ctt gag atc tcc gcg ttc att																355
Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile																85
cac gga caa aac ggc atc ggc gaa gtc gag ctg cca gca agc gag tca																403
His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser																100
aag gca ctc ccc ggc gca gtg gat ttc ctc att gat tcc gtc aac acc																451
Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr																115
cac ggc gat gac ctg gtg atc atc gca act ggt ccc atg acc aac ctg																499
His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly Pro Met Thr Asn Leu																120
tct gcg gca atc gca aag gat cca agc ttt gct tcc aag gct cac gtg																547
Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala Ser Lys Ala His Val																145
gtc atc atg ggt ggc gcc ttg act gtc cca ggc aac gtc agc aca tgg																595
Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly Asn Val Ser Thr Trp																165
gca gaa gca aac atc aac cag gac cca gat gca gca aac gat ctg ttc																643
Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala Ala Asn Asp Leu Phe																170

cgt tcc ggt gca gat gtc acc atg atc ggt ctt gat gtc acc ctg cag 691
 Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu Asp Val Thr Leu Gln
 185 190 195

acc ctt ctt acc aag aag cac act gcg cag tgg cgc gaa ctg ggc act 739
 Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp Arg Glu Leu Gly Thr
 200 205 210

cca gct gct atc gca ctg gcc gac atg act gat tac tac atc aag gca 787
 Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp Tyr Tyr Ile Lys Ala
 215 220 225

tat gag acc acc gca cca cac ctg ggc ggt tgc ggc ctg cac gac cca 835
 Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys Gly Leu His Asp Pro
 230 235 240 245

ctg gca gta ggc gtt gca gtg gac cca agc ctg gtc act ttg ctc ccc 883
 Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu Val Thr Leu Leu Pro
 250 255 260

atc aac ctc aag gta gac att gag ggc gag acc cgt gga cgc acc att 931
 Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr Arg Gly Arg Thr Ile
 265 270 275

ggc gat gaa gtc cgc ctc aac gat cca gtg cgc acc tcc cgc gca gct 979
 Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg Thr Ser Arg Ala Ala
 280 285 290

gtc gcc gta gac gtg gat cgt ttc ctt tct gaa ttc atg acc cgc atc 1027
 Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu Phe Met Thr Arg Ile
 295 300 305

ggc cga gtc gca gca cag cag taaaagcagc tctggtgaag gtt 1071
 Gly Arg Val Ala Ala Gln Gln
 310 315

<210> 1088

<211> 316

<212> PRT

<213> Corynebacterium glutamicum

<400> 1088

Met Ser Lys Lys Ala Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala
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Leu Ala Leu Ala Tyr Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly
 20 25 30

Val Thr Thr Thr Tyr Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn
 35 40 45

Asp Leu Ala Leu Leu Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr
 50 55 60

Leu Gly Glu Pro His Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu
 65 70 75 80

Ile Ser Ala Phe Ile His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu
 85 90 95

aaacattgtc ctccccattt cttgagtaag ggaaaatacc gtg gcc cgt gta gtt 115
Val Ala Arg Val Val
1 5

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gtc aat gtc atg cct aag gct gag att ctg gat ccc cag ggg cag gcg 163
Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp Pro Gln Gly Gln Ala
      10      15      20

gta cac cgc gcc ctc gga cgt atc gga gtt tct ggc gtt tcc gat gtc 211
Val His Arg Ala Leu Gly Arg Ile Gly Val Ser Gly Val Ser Asp Val
      25      30      35

cgt cag gga aag cgc ttc gag ctt gag gta gat gat tcc gtc acc gaa 259
Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp Asp Ser Val Thr Glu
      40      45      50

gct gac cta aag aaa att gct gaa acc ctc ctc gca aac acc gtc atc 307
Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu Ala Asn Thr Val Ile
      55      60      65

gaa gac ttc gat gtg gtg gga gtt gag gtc gcg aag tgagcgccaa 353
Glu Asp Phe Asp Val Val Gly Val Glu Val Ala Lys
      70      75      80

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<210> 1090

<211> 81

<212> PRT

<213> Corynebacterium glutamicum

<400> 1090

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Val Ala Arg Val Val Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp
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Pro Gln Gly Gln Ala Val His Arg Ala Leu Gly Arg Ile Gly Val Ser
      20      25      30

Gly Val Ser Asp Val Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp
      35      40      45

Asp Ser Val Thr Glu Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu
      50      55      60

Ala Asn Thr Val Ile Glu Asp Phe Asp Val Val Gly Val Glu Val Ala
      65      70      75      80

Lys

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<210> 1091

<211> 498

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(475)

<223> RXC00560

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catatggaca ctittaacggt tcgtactagg ctgatgcttc atg agg att gat ccg 115
Met Arg Ile Asp Pro
1 5

ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg 163
Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys Asp Trp Ile Glu Gly
10 15 20

gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act 211
Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala Leu Ala Ala Thr
25 30 35

cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg 259
Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala Pro Gly Asn Ser Val
40 45 50

gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca 307
Glu Val Arg Val Pro Pro Phe Val Ala Val Gln Cys Ile Glu Gly Pro
55 60 65

aaa cat aca cgc ggc aca cca ccc aac gtg gtg gag acc gac gcc aag 355
Lys His Thr Arg Gly Thr Pro Pro Asn Val Val Glu Thr Asp Ala Lys
70 75 80 85

acc tgg tta cgc tta gca cct ggg caa acc aca ttt gat gca gaa ttt 403
Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr Phe Asp Ala Glu Phe
90 95 100

gaa agc gga aaa att agc gca tca ggt acc cga gcc aaa gag att gcg 451
Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg Ala Lys Glu Ile Ala
105 110 115

gac tgg tta cca gtg gtc aaa ctt tagatttcct aatgctcatt agt 498
Asp Trp Leu Pro Val Val Lys Leu
120 125

<210> 1092

<211> 125

<212> PRT

<213> Corynebacterium glutamicum

<400> 1092

Met Arg Ile Asp Pro Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys
1 5 10 15

Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala
20 25 30

Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala
35 40 45

Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln
50 55 60

Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val
65 70 75 80

Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr
85 90 95

Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg
 100 105 110
 Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu
 115 120 125

<210> 1093
 <211> 1305
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1282)
 <223> RXC01088

<400> 1093
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 gtgaaccgaa ttttttaact gatttgaaga agcgagaata atg gga ctg tgg atc 115
 Met Gly Leu Trp Ile
 1 5
 gat gca acc gct ggc gtt gca ggg gat atg ttg ctg gga gca ctc att 163
 Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile
 10 15 20
 gat gca ggt gca gaa cta gaa aaa atc caa cag gtt gtg gaa gca gtc 211
 Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val
 25 30 35
 atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc 259
 Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly
 40 45 50
 caa cga ggc atc aag ctg cat gtg gac gca caa cat gaa cac cat cat 307
 Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His
 55 60 65
 cac cgc cac tta agc acc att aaa gaa ctg ctt gtc aat gct gac atc 355
 His Arg His Leu Ser Thr Ile Lys Glu Leu Leu Val Asn Ala Asp Ile
 70 75 80 85
 cct gaa caa acc aag cag gat gcc tta ggc gtt ttt gaa ctc atc gct 403
 Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val Phe Glu Leu Ile Ala
 90 95 100
 atc gct gaa gga aaa gtc cac ggc atc gag ccg gag aaa atc cac ttc 451
 Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro Glu Lys Ile His Phe
 105 110 115
 cat gag gta gga gct tgg gat tcc atc gca gac att gtg ggt gtg tgc 499
 His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp Ile Val Gly Val Cys
 120 125 130
 gaa gcg atc agg cag ctt aac cca ggt ttg att gct gca tct ccg att 547
 Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile Ala Ala Ser Pro Ile
 135 140 145
 gct tta gga ttc gga cgc atc aag gca gct cac gga gat att cca gtg 595

[illegible]

390

<210> 1094

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 1094

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Leu	Gly	Ala	Leu	Ile	Asp	Ala	Gly	Ala	Glu	Leu	Glu	Lys	Ile	Gln	Gln
			20					25					30		

Val	Val	Glu	Ala	Val	Ile	Pro	Gly	Asp	Val	Leu	Leu	Arg	Thr	Glu	Glu
		35					40					45			

Val	Val	Arg	Gln	Gly	Gln	Arg	Gly	Ile	Lys	Leu	His	Val	Asp	Ala	Gln
		50				55					60				

His	Glu	His	His	His	His	Arg	His	Leu	Ser	Thr	Ile	Lys	Glu	Leu	Leu
65					70					75					80

Val	Asn	Ala	Asp	Ile	Pro	Glu	Gln	Thr	Lys	Gln	Asp	Ala	Leu	Gly	Val
				85					90					95	

Phe	Glu	Leu	Ile	Ala	Ile	Ala	Glu	Gly	Lys	Val	His	Gly	Ile	Glu	Pro
			100					105					110		

Glu	Lys	Ile	His	Phe	His	Glu	Val	Gly	Ala	Trp	Asp	Ser	Ile	Ala	Asp
		115					120					125			

Ile	Val	Gly	Val	Cys	Glu	Ala	Ile	Arg	Gln	Leu	Asn	Pro	Gly	Leu	Ile
		130				135					140				

Ala	Ala	Ser	Pro	Ile	Ala	Leu	Gly	Phe	Gly	Arg	Ile	Lys	Ala	Ala	His
145					150					155					160

Gly	Asp	Ile	Pro	Val	Pro	Val	Pro	Ala	Val	Ala	Glu	Leu	Val	Lys	Gly
				165					170					175	

Trp	Pro	Thr	Gln	Thr	Gly	Ala	Leu	Met	Glu	Ser	Thr	Glu	Pro	Val	Gly
			180					185					190		

Glu	Leu	Ala	Thr	Pro	Thr	Gly	Val	Ala	Leu	Ile	Arg	His	Phe	Ala	Thr
		195					200					205			

Gln	Asp	Gly	Pro	Phe	Pro	Gly	Gly	Ile	Ile	Asn	Glu	Val	Gly	Ile	Gly
	210					215					220				

Ala	Gly	Thr	Lys	Asp	Thr	Glu	Gly	Arg	Pro	Asn	Ile	Val	Arg	Ala	Ile
225					230					235					240

Leu	Phe	Asn	Thr	Ser	Arg	Ser	Asn	Pro	Asp	Thr	Arg	Thr	Leu	Val	Gln
				245					250					255	

Leu	Glu	Ala	Asn	Val	Asp	Asp	Gln	Asp	Pro	Arg	Leu	Trp	Pro	Gly	Val
			260					265						270	

Ile	Glu	Ile	Leu	Phe	Ala	Ala	Gly	Ala	Val	Asp	Ala	Trp	Leu	Thr	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

275	280	285
Ile Leu Met Lys Lys Gly Arg Pro Ala His Arg Val Ser Ala Leu Val		
290	295	300
Asp Ser Ser Glu Val Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr		
305	310	315
Thr Thr Phe Gly Ile Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp		
	325	330
		335
Arg Arg Phe Glu Gln Val Glu Val Asp Gly His Thr Ile Asn Ile Lys		
	340	345
		350
Ile Gly Ser Arg Asp Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu		
	355	360
		365
Asp Ile Arg Ser Ala Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val		
	370	375
		380
Val Ala Arg Ile Pro Gln Gly Thr Thr Glu		
385	390	

<210> 1095

<211> 1419

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1396)

<223> RXC02624

<400> 1095

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                Val Leu Ile Pro His
                1                      5

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ggc gtg gcg gtg ctt ttg gtt att att ctc gcc gta gcc tcc cta atg 163
Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala Val Ala Ser Leu Met
                10                      15                      20

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ttc acc aat tct tca atg gtg aat ctt tgc gca acg att gca cag ctg 211
Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala Thr Ile Ala Gln Leu
                25                      30                      35

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tgg ctt tcc cta aat ctc ggt gcg gtg gac ggc agt ggg gaa gtg atc 259
Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly Ser Gly Glu Val Ile
                40                      45                      50

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tca gta ctg ccc acg ctt ccc ggc ttt ata ttc ctc tgg gcc atc gcc 307
Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe Leu Trp Ala Ile Ala
                55                      60                      65

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gcg cgc atc cac cgc gca gtc aaa gat cgt gtc agc atc gcc gac tta 355
Ala Arg Ile His Arg Ala Val Lys Asp Arg Val Ser Ile Ala Asp Leu
                70                      75                      80                      85

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ggc gtc ctc gca gca ctc gtc ctc ggc atc ccg ctt gcg ctc acc gcc	403
Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro Leu Ala Leu Thr Ala	
90 95 100	
atc gca gcg ttc atg ctt ttc gac gcc tcc agc gtc ctc aac gtc gag	451
Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser Val Leu Asn Val Glu	
105 110 115	
gtc ccg cca atc acg cgc ctc cta cgc gtg atg ttg ttc cac ctc agc	499
Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met Leu Phe His Leu Ser	
120 125 130	
gcc ctc ttc ctc ggc atg ggg cca cgc ctg tgg cag gcg ttg gcg cgc	547
Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp Gln Ala Leu Ala Arg	
135 140 145	
cgc tac ggt gct cca gaa tgg ctt atc gac gcc atc acc caa gct ttc	595
Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala Ile Thr Gln Ala Phe	
150 155 160 165	
cgc ttc ctc atc gca ttt gga aca gtc tcc ttg gtt tcc gtg ctc gtg	643
Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu Val Ser Val Leu Val	
170 175 180	
atg acc gcg atc aac cac agt gca ttc acc gcg acc atg cag ggt tac	691
Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala Thr Met Gln Gly Tyr	
185 190 195	
gac gac tcc gcc tct gtt gtg gcc ttg atc gtc ctg agc att ctg tat	739
Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val Leu Ser Ile Leu Tyr	
200 205 210	
ctg ccc aac atg atg atc ttt gcg atg ggc aat ctg atc ggc tca ccc	787
Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile Gly Ser Pro	
215 220 225	
ctt tac ttc ggt gac gcc tcc atc agc gtc ttc agc gtg cat tcc gtt	835
Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val His Ser Val	
230 235 240 245	
cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc gaa gcc ctc	883
Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser Glu Ala Leu	
250 255 260	
tca tgg gca gtg gcc tta ctg gtc atc cct gca att att gcc acc tgg	931
Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile Ala Thr Trp	
265 270 275	
gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca aca gca gca	979
Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr Thr Ala Ala	
280 285 290	
gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc gcc ggc gga	1027
Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe Ala Gly Gly	
295 300 305	
acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg gcg tca gtt	1075
Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu Ala Ser Val	
310 315 320 325	
ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc atc gcc gga	1123

Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu Ile Ala Gly
 330 335 340
 atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt aag gct gtg 1171
 Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val Lys Ala Val
 345 350 355
 gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac gaa gag gag 1219
 Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu
 360 365 370
 cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt gag gaa ggg 1267
 His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Val Glu Glu Gly
 375 380 385
 gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa gag aat cct 1315
 Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu Glu Asn Pro
 390 395 400 405
 gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act gag gct gaa 1363
 Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr Glu Ala Glu
 410 415 420
 gaa acc aat gat ggt tcc gag gcc gaa gac cgt taacatatct gttgtgaatt 1416
 Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
 425 430
 ctg 1419
 <210> 1096
 <211> 432
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1096
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 Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala
 20 25 30
 Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly
 35 40 45
 Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe
 50 55 60
 Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val
 65 70 75 80
 Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro
 85 90 95
 Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser
 100 105 110
 Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met
 115 120 125
 Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp

130	135	140
Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala 145 150 155 160		
Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu 165 170 175		
Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala 180 185 190		
Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val 195 200 205		
Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn 210 215 220		
Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe 225 230 235 240		
Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu 245 250 255		
Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala 260 265 270		
Ile Ile Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val 275 280 285		
Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala 290 295 300		
Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn 305 310 315 320		
Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly 325 330 335		
Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys 340 345 350		
Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu 355 360 365		
Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu 370 375 380		
Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp 385 390 395 400		
Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr 405 410 415		
Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg 420 425 430		

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<220>  
<221> CDS  
<222> (101) .. (580)  
<223> RXC02665
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caaggcgacc caatggcggtt taaagtaaca acccccattg atatgatgct ggcacaacgc 60

ggc 603

<210> 1098
<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 1098

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Val Thr Asn Pro Ile Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His
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Gln Ile Glu Ala Gly Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu
          20           25           30

Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His
          35           40           45

Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly
          50           55           60

Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr
          65           70           75           80

Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val
          85           90           95

Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly
          100          105          110

Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala
          115          120          125

Pro Cys Ser Leu Ser Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly
          130          135          140

Arg Ser Glu Gly Arg Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
          145          150          155          160

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<210> 1099

<211> 1689

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1666)

<223> RXC02770

<400> 1099

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tcgccggggc aaaaaccgta taattacagt cctattacga ttccggggaaa ggctgggtac 60

ttcacacatg ttgtttcgga agtcacgcag cgcggtaatc atg ttg gtt gca gcg 115
                                     Met Leu Val Ala Ala
                                     1           5

tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac 163
Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His
          10           15           20

caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc 211
Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr

```

25							30					35					
aac	gcg	gcg	tcg	ctg	ttg	gga	gtg	gct	aat	gat	gct	ggg	ctt	ttg	gct	259	
Asn	Ala	Ala	Ser	Leu	Leu	Gly	Val	Ala	Asn	Asp	Ala	Gly	Leu	Leu	Ala		
40						45						50					
gcc	aga	gtg	tat	ccg	ggg	gtg	tat	gtt	cag	ggg	cct	tct	ggg	cag	atg	307	
Ala	Arg	Val	Tyr	Pro	Gly	Val	Tyr	Val	Gln	Gly	Pro	Ser	Gly	Gln	Met		
55						60						65					
att	ccc	aac	act	gat	ctt	gct	tcc	acg	cag	gta	ttg	ccg	ggg	att	aac	355	
Ile	Pro	Asn	Thr	Asp	Leu	Ala	Ser	Thr	Gln	Val	Leu	Pro	Gly	Ile	Asn		
70						75						80			85		
cgc	cag	gtg	att	tac	act	atc	aat	gaa	gat	gcc	acc	tac	tca	gat	ggg	403	
Arg	Gln	Val	Ile	Tyr	Thr	Ile	Asn	Glu	Asp	Ala	Thr	Tyr	Ser	Asp	Gly		
			90						95						100		
cag	cct	gtg	gtg	tgt	gat	gat	ttt	ctg	ctc	tct	gcg	aca	gct	ggg	cag	451	
Gln	Pro	Val	Val	Cys	Asp	Asp	Phe	Leu	Leu	Ser	Ala	Thr	Ala	Gly	Gln		
			105						110						115		
atg	ccg	gaa	ctg	ttc	cag	tcc	cat	gtg	cca	ttg	acc	tcg	cag	att	gag	499	
Met	Pro	Glu	Leu	Phe	Gln	Ser	His	Val	Pro	Leu	Thr	Ser	Gln	Ile	Glu		
			120						125						130		
cga	gtg	gac	tgt	gta	tct	ggg	tct	aaa	gta	gcc	acc	gtg	gtg	ttc	aag	547	
Arg	Val	Asp	Cys	Val	Ser	Gly	Ser	Lys	Val	Ala	Thr	Val	Val	Phe	Lys		
135						140						145					
gaa	gac	ctc	ggg	gag	cgt	tgg	cgt	tat	ctt	ttt	gag	cag	ggc	gat	ttg	595	
Glu	Asp	Leu	Gly	Glu	Arg	Trp	Arg	Tyr	Leu	Phe	Glu	Gln	Gly	Asp	Leu		
150						155						160			165		
ttg	cca	gcc	cat	gcc	gtt	gct	tcc	aaa	gca	ggg	atg	acc	ttg	gag	gag	643	
Leu	Pro	Ala	His	Ala	Val	Ala	Ser	Lys	Ala	Gly	Met	Thr	Leu	Glu	Glu		
			170						175						180		
ctt	aat	cag	gcg	ttg	aag	gat	aag	gat	cct	gaa	gcg	ttg	act	gaa	cct	691	
Leu	Asn	Gln	Ala	Leu	Lys	Asp	Lys	Asp	Pro	Glu	Ala	Leu	Thr	Glu	Pro		
			185						190						195		
gct	cgt	gtg	tgg	agc	gaa	ggg	ttc	cag	ctg	tcc	cag	ttt	gat	cca	gag	739	
Ala	Arg	Val	Trp	Ser	Glu	Gly	Phe	Gln	Leu	Ser	Gln	Phe	Asp	Pro	Glu		
200						205						210					
ctg	cag	acg	gct	ttt	ggc	ccg	tac	aag	gtg	gat	tct	gtg	ggg	gaa	ttc	787	
Leu	Gln	Thr	Ala	Phe	Gly	Pro	Tyr	Lys	Val	Asp	Ser	Val	Gly	Glu	Phe		
215						220						225					
ggc	gaa	gtc	aag	ctg	gta	cgc	aat	gag	ttt	tac	agt	ggc	gac	cag	gcg	835	
Gly	Glu	Val	Lys	Leu	Val	Arg	Asn	Glu	Phe	Tyr	Ser	Gly	Asp	Gln	Ala		
230						235						240			245		
gtt	gaa	gca	gaa	atc	acg	atg	tgg	cct	aaa	ggc	tcg	gat	ctc	agc	gcc	883	
Val	Glu	Ala	Glu	Ile	Thr	Met	Trp	Pro	Lys	Gly	Ser	Asp	Leu	Ser	Ala		
			250						255						260		
att	gcg	gat	aat	gga	aac	ctt	cag	atc	gca	cat	gtt	gtg	gcg	tgg	gag	931	
Ile	Ala	Asp	Asn	Gly	Asn	Leu	Gln	Ile	Ala	His	Val	Val	Ala	Trp	Glu		
			265						270						275		

agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct tat gac att	979
Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile	
280 285 290	
aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc	1027
Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala	
295 300 305	
ggt gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg gcc tgc gtt	1075
Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val	
310 315 320 325	
gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat	1123
Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp	
330 335 340	
gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg	1171
Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val	
345 350 355	
cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat	1219
His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn	
360 365 370	
gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga	1267
Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly	
375 380 385	
ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt	1315
Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys	
390 395 400 405	
gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt	1363
Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser	
410 415 420	
ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag	1411
Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln	
425 430 435	
tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat	1459
Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His	
440 445 450	
cgg gag tat gaa aat gcc aat acc att gga act gat gcg gag tcg acg	1507
Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr	
455 460 465	
agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta	1555
Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu	
470 475 480 485	
gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc ggt aac gtt	1603
Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val	
490 495 500	
gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg gac cgt tgg	1651
Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp	
505 510 515	

tcc aga agt gag gaa taagtagtga gccaacaagc tct
 Ser Arg Ser Glu Glu
 520

1689

<210> 1100

<211> 522

<212> PRT

<213> Corynebacterium glutamicum

<400> 1100

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Glu Pro Thr Ser His Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser
 20 25 30

Ser Leu Ala Thr Thr Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp
 35 40 45

Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly
 50 55 60

Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val
 65 70 75 80

Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala
 85 90 95

Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser
 100 105 110

Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu
 115 120 125

Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala
 130 135 140

Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe
 145 150 155 160

Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly
 165 170 175

Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu
 180 185 190

Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser
 195 200 205

Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp
 210 215 220

Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr
 225 230 235 240

Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly
 245 250 255

Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His
 260 265 270

Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu
 275 280 285
 Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu
 290 295 300
 Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala
 305 310 315 320
 Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser
 325 330 335
 Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His
 340 345 350
 Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met
 355 360 365
 Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg
 370 375 380
 Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala
 385 390 395 400
 Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser
 405 410 415
 Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu
 420 425 430
 Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg
 435 440 445
 Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr
 450 455 460
 Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val
 465 470 475 480
 Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg
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 500 505 510
 Asn Met Asp Arg Trp Ser Arg Ser Glu Glu
 515 520

<210> 1101

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> RXC02238

<400> 1101

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                               Val Thr Asn Val Ser
                               1      5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
                10                15                20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
                25                30                35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
                40                45                50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
                55                60                65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
                70                75                80                85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
                90                95

cac 408

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<210> 1102

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1102

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Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
  20      25      30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
  35      40      45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
  50      55      60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
  65      70      75      80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
  85      90      95

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<210> 1103

<211> 1298

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1275)

<223> RXC01946

<400> 1103

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tac gaa gct gac gcc gaa gca gcc cag atc tgc gac aac ctc ggc ctc	96
Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu	
20 25 30	
gag gca cgc atc ctc gac cag cag ctt aaa acc ctg tcc ggc ggc cag	144
Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln	
35 40 45	
cgc cgc cgc gtc gag ttg gcg cag atc ctc ttc gcc gcc acc aac ggc	192
Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly	
50 55 60	
tcc ggc aaa tca aaa acc aca ttg ctt ctc gac gag ccc acc aac cac	240
Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His	
65 70 75 80	
ttg gac gca gac tcg atc acc tgg ctc cgt gac ttc ctg gcg aag cac	288
Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His	
85 90 95	
gaa ggt gga ctg atc atg att tcg cac gac gtc gaa ctg ctt ggc gcc	336
Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala	
100 105 110	
gta tgt aac aag att tgg tac ctc gac gca gta cgc agc gaa gcc gat	384
Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp	
115 120 125	
gtc tac aac atg ggc ttt agc aaa tac gtc gat gca cgt gca ctc gat	432
Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp	
130 135 140	
gaa gca cgc cga cgc cgt gag cgc gca aac gcc gaa aag aag gcc gga	480
Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly	
145 150 155 160	
gcc ctc aag gac cag gct gca cgc ctc ggc gcg aaa gca acc aag gct	528
Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala	
165 170 175	
gcc gca gct aag cag atg atc gcc cgt gcg gaa cga atg atc gac aac	576
Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn	
180 185 190	
ctc gac gaa atc cgc gta gct gac cgc gcc gcc aac atc gtt ttc cca	624
Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro	
195 200 205	
gaa cca gca ccc tgt gga aaa acc cca ctc aac gcc aag ggc ctg acc	672

Glu	Pro	Ala	Pro	Cys	Gly	Lys	Thr	Pro	Leu	Asn	Ala	Lys	Gly	Leu	Thr	
210						215					220					
aag	atg	tac	ggc	tcc	ctc	gaa	gtc	ttc	gcc	ggc	gtc	gac	cta	gcc	atc	720
Lys	Met	Tyr	Gly	Ser	Leu	Glu	Val	Phe	Ala	Gly	Val	Asp	Leu	Ala	Ile	
225					230					235					240	
gac	aaa	ggc	tcc	cgc	gta	gtc	gtc	ctc	gga	ttc	aac	ggt	gca	ggt	aaa	768
Asp	Lys	Gly	Ser	Arg	Val	Val	Val	Leu	Gly	Phe	Asn	Gly	Ala	Gly	Lys	
				245					250					255		
acc	acc	ctg	ctc	aaa	ctc	ctc	gcc	ggt	gtg	gaa	cgc	acc	gac	ggc	gaa	816
Thr	Thr	Leu	Leu	Lys	Leu	Leu	Ala	Gly	Val	Glu	Arg	Thr	Asp	Gly	Glu	
			260					265					270			
ggc	ggc	atc	gtc	acc	gga	tac	ggc	ctc	aaa	atc	ggc	tac	ttc	gcc	cag	864
Gly	Gly	Ile	Val	Thr	Gly	Tyr	Gly	Leu	Lys	Ile	Gly	Tyr	Phe	Ala	Gln	
		275					280					285				
gaa	cac	gac	acc	atc	gac	ccc	gac	aaa	tcc	gtc	tgg	caa	aac	acc	atc	912
Glu	His	Asp	Thr	Ile	Asp	Pro	Asp	Lys	Ser	Val	Trp	Gln	Asn	Thr	Ile	
	290					295					300					
gaa	gcc	tgc	gcc	gac	gcc	gac	caa	caa	agc	ctc	cgc	agc	ctc	ctc	gga	960
Glu	Ala	Cys	Ala	Asp	Ala	Asp	Gln	Gln	Ser	Leu	Arg	Ser	Leu	Leu	Gly	
305					310					315					320	
tcc	ttc	atg	ttc	tcc	ggc	gaa	caa	ctc	gac	caa	cca	gca	gga	aca	ctc	1008
Ser	Phe	Met	Phe	Ser	Gly	Glu	Gln	Leu	Asp	Gln	Pro	Ala	Gly	Thr	Leu	
				325					330					335		
tcc	ggc	ggt	gaa	aaa	acc	cgc	ctc	gca	ctg	gcc	acc	ctc	gtg	tcc	tcc	1056
Ser	Gly	Gly	Glu	Lys	Thr	Arg	Leu	Ala	Leu	Ala	Thr	Leu	Val	Ser	Ser	
			340					345					350			
cgc	gca	aac	gtc	ctg	ctt	ctc	gac	gag	ccc	acc	aac	aac	ctt	gac	ccg	1104
Arg	Ala	Asn	Val	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	Asn	Leu	Asp	Pro	
		355					360					365				
atc	tcc	cgc	gaa	cag	gtc	ctc	gac	gca	ctg	cgc	acc	tac	acc	ggc	gca	1152
Ile	Ser	Arg	Glu	Gln	Val	Leu	Asp	Ala	Leu	Arg	Thr	Tyr	Thr	Gly	Ala	
	370					375					380					
gtc	gtc	ctg	gtt	acc	cac	gac	ccg	ggt	gca	gtc	aag	gcc	ctt	gag	cca	1200
Val	Val	Leu	Val	Thr	His	Asp	Pro	Gly	Ala	Val	Lys	Ala	Leu	Glu	Pro	
385					390					395					400	
gaa	cgc	gtc	atc	gtg	ctt	cct	gat	ggc	acc	gag	gat	ctt	tgg	aat	gat	1248
Glu	Arg	Val	Ile	Val	Leu	Pro	Asp	Gly	Thr	Glu	Asp	Leu	Trp	Asn	Asp	
				405					410					415		
cag	tac	atg	gaa	atc	gtg	gaa	ttg	gcg	taggttctaa	ggctgtttat						1295
Gln	Tyr	Met	Glu	Ile	Val	Glu	Leu	Ala								
			420				425									
gct																1298

<210> 1104

<211> 425

<212> PRT

<213> Corynebacterium glutamicum

<400> 1104

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Ile Arg Lys Tyr Ser Arg Leu Glu Glu Gln Phe Gln Ser Leu Gly Gly
 1           5           10           15

Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu
      20           25           30

Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln
      35           40           45

Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly
      50           55           60

Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His
      65           70           75           80

Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His
      85           90           95

Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala
      100          105          110

Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp
      115          120          125

Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp
      130          135          140

Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly
      145          150          155          160

Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala
      165          170          175

Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn
      180          185          190

Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro
      195          200          205

Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr
      210          215          220

Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile
      225          230          235          240

Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys
      245          250          255

Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu
      260          265          270

Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln
      275          280          285

Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile
      290          295          300

Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly

```

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<210> 1105
<211> 613
<212> DNA
<213> Corynebacterium glutamicum
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<400> 1105
atacttttgtt ggactggaaa agtggccggtt tggttccctc caagcccaaa ttcqcccgcg 60

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
10 15 20

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
40 45 50

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ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca    355
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
  70                      75                      80                      85

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gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
 150 155 160 165

gac gca ttg gcg gaa tct 613
 Asp Ala Leu Ala Glu Ser
 170

<210> 1106

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1106

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
 1 5 10 15

Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
 20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
 130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
 145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
 165 170

<210> 1107

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> FRXA02857

<400> 1107

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cggtcttctt ctgggcgggca atgatttaac atgtgaagct atg gac atc acc atc 115
Met Asp Ile Thr Ile
1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
150 155 160 165

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613

gac gca ttg gcg gaa tct
 Asp Ala Leu Ala Glu Ser
 170

<210> 1108

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1108

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
 1 5 10 15

Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
 20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
 130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
 145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
 165 170

<210> 1109

<211> 424

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(424)

<223> RXN00450

<400> 1109

tttgcgatga catggatttg gatccttccg aacaattgct gcgcatcgcg gaagaactcg 60

gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
 Val Gly Val Leu Pro
 1 5

```

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
      10      15      20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
      25      30      35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
      40      45      50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
      55      60      65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
      70      75      80      85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
      90      95      100

ggt gct cga atc gga cgc atc 424
Gly Ala Arg Ile Gly Arg Ile
      105

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<210> 1110

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1110

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Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
  1      5      10      15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
      20      25      30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
      35      40      45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
      50      55      60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
      65      70      75      80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
      85      90      95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
      100      105

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<210> 1111

<211> 418

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> FRXA00450

<400> 1111

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
                                         Val Gly Val Leu Pro
                                         1                               5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
                        10                        15                        20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
                        25                        30                        35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
                        40                        45                        50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
                        55                        60                        65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
                        70                        75                        80                        85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
                        90                        95                        100

ggg gct cga atc gga
Gly Ala Arg Ile Gly
                        105

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<210> 1112

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 1112

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Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
  1                               5                               10                               15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
      20                        25                        30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
      35                        40                        45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
      50                        55                        60

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Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
 65 70 75 80
 Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
 85 90 95
 Ala Gly Ala Leu Val Gly Ala Arg Ile Gly
 100 105

<210> 1113

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA00465

<400> 1113

tccccaacgc gcaccgaact tagccggatc gcagacttca cctggatgtc caccgcagcc 60
 caagcgctac cagcgttgat gcgaggtttg agcgcctaac atg act gaa gat gac 115
 Met Thr Glu Asp Asp
 1 5
 tta gat ctg ctg cac cgc aca gta gaa cta gcc acc cag gca ctc aag 163
 Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala Thr Gln Ala Leu Lys
 10 15 20
 cag gga aac agt cct tat gga tcc ctg ctg gtt gat ccc ttc ggc gcg 211
 Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val Asp Pro Phe Gly Ala
 25 30 35
 gtc gtt ttt gaa gac cac aac cga gat gcc gat ggg gat ctg acc aag 259
 Val Val Phe Glu Asp His Asn Arg Asp Ala Asp Gly Asp Leu Thr Lys
 40 45 50
 cac ccg gaa ttc gcc atc gcc aaa tat gcg atc gaa aat tac agt gca 307
 His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile Glu Asn Tyr Ser Ala
 55 60 65
 tca gaa cgt gct gcg tgc act gtt tat acc tcg acg gaa cat tgc gcg 355
 Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser Thr Glu His Cys Ala
 70 75 80 85
 atg tgc gcc ggt gcc cat gcg tgg gct gga ctg ggc aaa att tac tgc 403
 Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu Gly Lys Ile Tyr Cys
 90 95 100
 gcc acc aca ggt ggg caa aca gcc gct tgg tac gca aag tgg ggt gca 451
 Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr Ala Lys Trp Gly Ala
 105 110 115
 gaa tct ggg cct ttg aac ccg att tca gcg gac aaa att agc ccg aac 499
 Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp Lys Ile Ser Pro Asn
 120 125 130
 ata tcc atc gaa gga cct gct tcc aga ttt gag gaa gtc ctg tat gaa 547
 Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu Glu Val Leu Tyr Glu

135 140 145
 ctg cat cga tgg ttt tat tta ggg cag tct ccg aat aag gct ctt 592
 Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro Asn Lys Ala Leu
 150 155 160

tagcgctggg catgtgactt taa 615

<210> 1114
 <211> 164
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1114
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Thr Gln Ala Leu Lys Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val
 20 25 30

Asp Pro Phe Gly Ala Val Val Phe Glu Asp His Asn Arg Asp Ala Asp
 35 40 45

Gly Asp Leu Thr Lys His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile
 50 55 60

Glu Asn Tyr Ser Ala Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser
 65 70 75 80

Thr Glu His Cys Ala Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu
 85 90 95

Gly Lys Ile Tyr Cys Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr
 100 105 110

Ala Lys Trp Gly Ala Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp
 115 120 125

Lys Ile Ser Pro Asn Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu
 130 135 140

Glu Val Leu Tyr Glu Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro
 145 150 155 160

Asn Lys Ala Leu

<210> 1115
 <211> 1083
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1060)
 <223> RXA00717

<400> 1115
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act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc 787
Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser
215 220 225

gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac 835
 Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp
 230 235 240 245

ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc 883
 Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile
 250 255 260

gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag 931
 Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu
 265 270 275

ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt 979
 Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val
 280 285 290

cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct 1027
 Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser
 295 300 305

gag ctg acc agc tta tac aag gtg gtc caa ctg tgacggaaat ttccaacatg 1080
 Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu
 310 315 320

cct 1083

<210> 1116
 <211> 320
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1116
 Val Thr Pro Pro Ala Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser
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 Asn Arg Ser Gly Gly Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly
 20 25 30
 Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile
 35 40 45
 Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp
 50 55 60
 Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val
 65 70 75 80
 Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His
 85 90 95
 Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile
 100 105 110
 Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg
 115 120 125
 Val Asp Gly Val Arg Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val
 130 135 140
 Leu Asn Lys Pro Arg Gly Met His Ser Thr Met Ser Asp Glu Leu Gly

145		150		155		160
Arg Pro Cys Val	Gly Asp Leu Val	Ser Glu Lys Thr	Ala Ser Gly Gln			
	165	170	175			
Arg Leu Phe His	Val Gly Arg Leu	Asp Ala Asp Thr	Glu Gly Leu Leu			
	180	185	190			
Leu Leu Thr Asn	Asp Gly Glu Leu	Ala Asn Arg Leu	Met His Pro Lys			
	195	200	205			
Tyr Glu Val Ser	Lys Thr Tyr Leu	Ala Thr Val Arg	Gly Glu Ala Thr			
	210	215	220			
Asn Lys Leu Val	Ser Ala Leu Arg	Asp Gly Val Glu	Leu Glu Asp Gly			
	225	230	235	240		
Pro Ala Lys Ala	Asp Phe Ala Gln	Ile Ile Asp Val	Phe Gln Gly Lys			
	245	250	255			
Ser Leu Leu Arg	Ile Glu Ile His	Glu Gly Arg Lys	His Ile Val Arg			
	260	265	270			
Arg Leu Phe Asp	Glu Leu Gly Phe	Pro Val Glu Arg	Leu Val Arg Thr			
	275	280	285			
Lys Leu His Thr	Val Gln Leu Gly	Asp Gln Lys Pro	Gly Ser Leu Arg			
	290	295	300			
Ala Leu Asn Ser	Ser Glu Leu Thr	Ser Leu Tyr Lys	Val Val Gln Leu			
	305	310	315	320		

<210> 1117

<211> 978

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(955)

<223> RXA01894

<400> 1117

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				Met Pro Lys Pro Lys	
				1 5	

aat aat gcg ggt	cga gat ctc	aaa gct gcc	att gct gtg	ggg atc gga	163
Asn Asn Ala Gly	Arg Asp Leu	Lys Ala Ala	Ile Ala Val	Gly Ile Gly	
	10	15	20		

ctg ggg gtc	ctg gtt ctt	ttg ggg att	gtc cta agc	cca tgg ggt	211
Leu Gly Val	Leu Val Leu	Leu Gly Ile	Val Leu Ser	Pro Trp Gly	
	25	30	35		

tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt	259
Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly	
40 45 50	
agc aga ctt aaa gaa ggc ggc tat cat ttg cca ctg ccg att atg atc	307
Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met Ile	
55 60 65	
atc ggc ggt cag gca atc atc tgg ctg tca tgg cca ttt ggc acg atg	355
Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr Met	
70 75 80 85	
ggc att ttg gcg tct ttt gtg gcc act gtg ttg gtg ctg atg tat ttc	403
Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr Phe	
90 95 100	
cga att ttc tac aat ggc acg gaa aaa gaa gcc cgc aac tat ttg agg	451
Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu Arg	
105 110 115	
gac acc tct gtg ggc atc ttc gtg ctc acc tgg att cca ttg ttc gga	499
Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe Gly	
120 125 130	
agc ttc gct gcg atg ctg tcg ctg atg caa aac aat tcc atc ccg ggt	547
Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro Gly	
135 140 145	
aca tat ttc att ttg acg ttc atg ctg tgt gtg atc gca tcg gat gtg	595
Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp Val	
150 155 160 165	
ggc ggg tat atc gcg ggt gtg ttc ttt gga tcg cac cca atg gcg ccg	643
Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala Pro	
170 175 180	
ttg gtg agt ccg aag aag tct tgg gaa ggc ttt gcc ggc tcc att gtc	691
Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile Val	
185 190 195	
tta gga tcg gtc act ggt gca ctc agt gtt cac ttc ctg ctc gat cac	739
Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp His	
200 205 210	
cac tgg tgg atg ggt gtg atc ttg ggt tgt gcc cta gtt gtg tgc gcc	787
His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys Ala	
215 220 225	
acg ttg ggt gac ttg gtt gag tcg cag ttc aaa cgc gat ttg ggc atc	835
Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly Ile	
230 235 240 245	
aag gat atg tcg aac ctt ctt cca ggc cac ggc gga ttg atg gac cgt	883
Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp Arg	
250 255 260	
ttg gat ggc atg ctc ccg gcc gcg atg gtg acg tgg ttg atc ctg agt	931
Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu Ser	
265 270 275	
gtg atc agc agc tcg tat ccg tcg taaagcttgg gccagcttta agt	978

Val Ile Ser Ser Ser Tyr Pro Ser
280 285

<210> 1118

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 1118

Met Pro Lys Pro Lys Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile
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Ala Val Gly Ile Gly Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu
20 25 30

Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala
35 40 45

Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro
50 55 60

Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp
65 70 75 80

Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu
85 90 95

Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala
100 105 110

Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp
115 120 125

Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn
130 135 140

Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val
145 150 155 160

Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser
165 170 175

His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe
180 185 190

Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His
195 200 205

Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala
210 215 220

Leu Val Val Cys Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys
225 230 235 240

Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly
245 250 255

Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr
260 265 270

Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser
 275 280 285

<210> 1119

<211> 879

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> RXA02536

<400> 1119

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gcgtattgcc ttgcttcaga tctcgacgaa ttccgataag atg gac aac ttc gcc 115
 Met Asp Asn Phe Ala
 1 5

ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163
 Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val
 10 15 20

ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211
 Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu
 25 30 35

gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259
 Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg
 40 45 50

aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307
 Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr
 55 60 65

cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355
 Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn
 70 75 80 85

aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403
 Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys
 90 95 100

att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451
 Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys
 105 110 115

ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499
 Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly
 120 125 130

gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547
 Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu
 135 140 145

gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac 595
 Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp
 150 155 160 165

ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca 643
 Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala
 170 175 180

ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca 691
 Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro
 185 190 195

gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc 739
 Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser
 200 205 210

atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag 787
 Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu
 215 220 225

cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att 835
 Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile
 230 235 240 245

cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act 879
 Arg Glu Ala Leu Pro Val Leu
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<210> 1120

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 1120

Met Asp Asn Phe Ala Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu
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Gln Gly Ala Arg Val Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe
 20 25 30

Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe
 35 40 45

Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val
 50 55 60

Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr
 65 70 75 80

Ile Ser Arg Val Asn Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His
 85 90 95

Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu
 100 105 110

Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp
 115 120 125

Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu
 130 135 140

Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro
 145 150 155 160

Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu
 165 170 175
 Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly
 180 185 190
 Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr
 195 200 205
 Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala
 210 215 220
 Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser
 225 230 235 240
 Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu
 245 250

<210> 1121

<211> 1528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> RXN01209

<400> 1121

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ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115
 Met Cys Glu Arg Pro
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
 25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val
 40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307
 Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala
 55 60 65

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355
 Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu
 70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403
 Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln
 90 95 100

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451

Ala	Arg	Glu	Leu	Leu	Pro	Ala	His	Leu	Glu	Leu	Gly	Leu	Ser	Ile	Glu		
			105					110					115				
aac	ctg	gat	caa	ttg	cat	gct	gtg	atc	gcg	cag	tgc	gcc	gag	act	ggt	499	
Asn	Leu	Asp	Gln	Leu	His	Ala	Val	Ile	Ala	Gln	Cys	Ala	Glu	Thr	Gly		
		120					125					130					
gtg	gca	ttg	ccc	gat	gtg	att	ggc	att	ggt	ccg	gtg	gcc	tct	act	gcg	547	
Val	Ala	Leu	Pro	Asp	Val	Ile	Gly	Ile	Gly	Pro	Val	Ala	Ser	Thr	Ala		
		135				140					145						
acc	aaa	cca	gat	gcg	gca	ccc	gca	ttg	ggt	gtg	gag	ggc	atc	gct	gag	595	
Thr	Lys	Pro	Asp	Ala	Ala	Pro	Ala	Leu	Gly	Val	Glu	Gly	Ile	Ala	Glu		
		150			155					160					165		
atc	gcc	gct	gta	gct	caa	gac	cac	ggc	atc	gca	tca	gta	gct	att	gga	643	
Ile	Ala	Ala	Val	Ala	Gln	Asp	His	Gly	Ile	Ala	Ser	Val	Ala	Ile	Gly		
				170					175					180			
ggc	gtt	ggt	cta	cgc	aac	gcg	gcc	gaa	ctc	gct	gct	acg	ccc	atc	gac	691	
Gly	Val	Gly	Leu	Arg	Asn	Ala	Ala	Glu	Leu	Ala	Ala	Thr	Pro	Ile	Asp		
			185					190					195				
ggt	ctg	tgc	gtg	gtc	tct	gaa	atc	atg	acc	gcc	gcc	aat	cca	gca	gct	739	
Gly	Leu	Cys	Val	Val	Ser	Glu	Ile	Met	Thr	Ala	Ala	Asn	Pro	Ala	Ala		
		200				205						210					
gcg	gca	act	cgc	ctg	cgg	act	gct	ttt	caa	cct	act	ttc	tcg	cct	gaa	787	
Ala	Ala	Thr	Arg	Leu	Arg	Thr	Ala	Phe	Gln	Pro	Thr	Phe	Ser	Pro	Glu		
		215				220					225						
act	caa	act	gaa	ctc	tct	caa	aca	gaa	ctc	caa	gga	gcc	ttc	gtg	aat	835	
Thr	Gln	Thr	Glu	Leu	Ser	Gln	Thr	Glu	Leu	Gln	Gly	Ala	Phe	Val	Asn		
		230			235					240					245		
tcg	cct	tct	gcc	cca	cgt	gtg	ttg	tct	att	gca	ggc	act	gat	ccc	aca	883	
Ser	Pro	Ser	Ala	Pro	Arg	Val	Leu	Ser	Ile	Ala	Gly	Thr	Asp	Pro	Thr		
				250					255					260			
ggt	ggt	gca	ggt	att	cag	gct	gat	ctg	aag	tcc	att	gca	gca	ggt	ggc	931	
Gly	Gly	Ala	Gly	Ile	Gln	Ala	Asp	Leu	Lys	Ser	Ile	Ala	Ala	Gly	Gly		
			265					270					275				
ggc	tac	ggc	atg	tgc	gtt	gtg	acc	tcg	ctg	gtc	gcg	caa	aac	acc	cac	979	
Gly	Tyr	Gly	Met	Cys	Val	Val	Thr	Ser	Leu	Val	Ala	Gln	Asn	Thr	His		
		280					285					290					
ggc	gtc	aac	acg	atc	cac	acc	cca	ccc	ttg	acc	ttt	ttg	gaa	gaa	cag	1027	
Gly	Val	Asn	Thr	Ile	His	Thr	Pro	Pro	Leu	Thr	Phe	Leu	Glu	Glu	Gln		
		295				300					305						
ctg	gaa	gcg	gtc	ttt	tcc	gat	gtc	acc	gtc	gat	gcc	atc	aag	ctc	ggc	1075	
Leu	Glu	Ala	Val	Phe	Ser	Asp	Val	Thr	Val	Asp	Ala	Ile	Lys	Leu	Gly		
					315				320						325		
atg	ttg	ggc	tct	gcc	gac	acc	gtc	gat	ctg	gtg	gct	tca	tgg	ctt	ggt	1123	
Met	Leu	Gly	Ser	Ala	Asp	Thr	Val	Asp	Leu	Val	Ala	Ser	Trp	Leu	Gly		
				330					335					340			
tcc	cac	gag	cac	ggt	ccc	gtg	gtg	ctt	gat	ccc	gtc	atg	atc	gcc	acc	1171	
Ser	His	Glu	His	Gly	Pro	Val	Val	Leu	Asp	Pro	Val	Met	Ile	Ala	Thr		

345						350						355						
agc	ggt	gat	cgc	cta	ctg	gat	gcg	agc	gct	gaa	gaa	tcg	ctg	cgc	cgc	1219		
Ser	Gly	Asp	Arg	Leu	Leu	Asp	Ala	Ser	Ala	Glu	Glu	Ser	Leu	Arg	Arg			
360						365						370						
ctg	gcc	gtg	cac	gtc	gat	gtg	gtc	acc	ccg	aat	atc	ccc	gaa	ctt	gcc	1267		
Leu	Ala	Val	His	Val	Asp	Val	Val	Thr	Pro	Asn	Ile	Pro	Glu	Leu	Ala			
375						380						385						
gtg	ttg	tgc	gac	agt	gct	cct	gcc	atc	acc	atg	gat	gag	gcc	att	gct	1315		
Val	Leu	Cys	Asp	Ser	Ala	Pro	Ala	Ile	Thr	Met	Asp	Glu	Ala	Ile	Ala			
390						395						400						405
cag	gct	cag	gga	ttt	gcg	cgg	act	cat	gac	acc	atc	gtc	att	gtc	aag	1363		
Gln	Ala	Gln	Gly	Phe	Ala	Arg	Thr	His	Asp	Thr	Ile	Val	Ile	Val	Lys			
410						415						420						
ggt	gga	cat	ctg	act	ggc	gcg	ctt	gct	gat	aac	gct	gtc	gtg	cgc	ccc	1411		
Gly	Gly	His	Leu	Thr	Gly	Ala	Leu	Ala	Asp	Asn	Ala	Val	Val	Arg	Pro			
425						430						435						
gac	ggc	tcg	gtg	ttc	cag	gtg	gaa	aac	ctg	cgt	gtc	aac	acc	acc	aac	1459		
Asp	Gly	Ser	Val	Phe	Gln	Val	Glu	Asn	Leu	Arg	Val	Asn	Thr	Thr	Asn			
440						445						450						
tcc	cat	ggc	aca	ggc	tgt	tcg	ctc	tct	gcg	tca	ctt	gcc	acc	aag	atc	1507		
Ser	His	Gly	Thr	Gly	Cys	Ser	Leu	Ser	Ala	Ser	Leu	Ala	Thr	Lys	Ile			
455						460						465						
gcc	gcc	ggc	gaa	agc	gtg	gaa										1528		
Ala	Ala	Gly	Glu	Ser	Val	Glu												
470						475												

<210> 1122

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1122

Met	Cys	Glu	Arg	Pro	Glu	Lys	Tyr	Val	Thr	Asp	Phe	Ser	Leu	Tyr	Leu
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Val	Thr	Asp	Pro	Val	Leu	Gly	Gly	Gly	Pro	Lys	Lys	Val	Ala	Gly	Ile
		20					25						30		

Val	Asp	Ser	Ala	Ile	Ser	Gly	Gly	Val	Ser	Val	Val	Gln	Leu	Arg	Asp
	35					40						45			

Lys	Asn	Ser	Gly	Val	Glu	Asp	Val	Arg	Ala	Ala	Ala	Lys	Glu	Leu	Lys
	50					55					60				

Glu	Leu	Cys	Asp	Ala	Arg	Gly	Val	Ala	Leu	Val	Val	Asn	Asp	Tyr	Leu
65					70					75				80	

Asp	Ile	Ala	Val	Glu	Leu	Gly	Leu	His	Leu	His	Ile	Gly	Gln	Gly	Asp
			85					90						95	

Thr	Pro	Tyr	Thr	Gln	Ala	Arg	Glu	Leu	Leu	Pro	Ala	His	Leu	Glu	Leu
			100					105					110		

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
 435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
 450 455 460

Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
 465 470 475

<210> 1123

<211> 1528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> FRXA01209

<400> 1123

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ctttatgacg tggatgcccc ggctgtggcc tcgttggttg atg tgc gag agg cct 115
 Met Cys Glu Arg Pro
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
 25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val
 40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307
 Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala
 55 60 65

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355
 Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu
 70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403
 Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln
 90 95 100

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451
 Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu
 105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt 499
 Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly
 120 125 130

gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg 547
 Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala

135	140	145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu 150 155 160 165			595
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly 170 175 180			643
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp 185 190 195			691
ggc ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala 200 205 210			739
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu 215 220 225			787
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn 230 235 240 245			835
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr 250 255 260			883
ggc ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly 265 270 275			931
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His 280 285 290			979
ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln 295 300 305			1027
ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly 310 315 320 325			1075
atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly 330 335 340			1123
tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr 345 350 355			1171
agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg 360 365 370			1219
ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala 375 380 385			1267

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag 1363
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc 1411
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac 1459
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc 1507
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
 455 460 465

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<210> 1124

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1124

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 20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
 35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
 50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
 65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
 85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
 100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430
 Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
 435 440 445
 Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
 450 455 460
 Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
 465 470 475

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 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(772)
 <223> RXN01617

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 Leu Ile Leu Lys Thr
 1 5
 act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163
 Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn
 10 15 20
 cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211
 Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile
 25 30 35
 ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259
 Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu
 40 45 50
 gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc 307
 Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys
 55 60 65
 aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc 355
 Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg
 70 75 80 85
 gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag 403
 Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu
 90 95 100
 gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg 451
 Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu
 105 110 115
 aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt 499
 Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val
 120 125 130
 gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt 547
 Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu
 135 140 145
 ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac 595
 Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp
 150 155 160 165
 gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca 643
 Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala
 170 175 180

cct 795

<213> Corynebacterium glutamicum

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Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 210 215 220

<210> 1127
 <211> 638
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(615)
 <223> FRXA01617

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 Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
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 aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc 96
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30
 gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg 144
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
 35 40 45
 atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc 192
 Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala
 50 55 60
 ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac 240
 Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn
 65 70 75 80
 ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac 288
 Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
 85 90 95
 gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac 336
 Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
 100 105 110
 gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac 384
 Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
 115 120 125
 gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc 432
 Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile
 130 135 140
 ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc 480
 Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
 145 150 155 160
 acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc 528
 Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
 165 170 175

gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac 576
 Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
 180 185 190

gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt 625
 Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 195 200 205

aaacaagctc cct 638

<210> 1128

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 1128

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Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
 35 40 45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala
 50 55 60

Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn
 65 70 75 80

Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
 85 90 95

Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
 100 105 110

Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
 115 120 125

Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile
 130 135 140

Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
 145 150 155 160

Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
 165 170 175

Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
 180 185 190

Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 195 200 205

<210> 1129

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXC01600

<400> 1129

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tttggagctg cgtgtccacc cttagatcta caatgtgatc atg gtt tcg aag atg 115
                                         Met Val Ser Lys Met
                                         1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163
His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu
                        10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211
Leu Glu Ser Pro Ile Leu Gly Val Arg Asp Ser Leu Ile Met Pro
                        25 30 35

ggg ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259
Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val
                        40 45 50

gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307
Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr
                        55 60 65

cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355
Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu
                        70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403
Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met
                        90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451
Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu
                        105 110 115

att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499
Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala
                        120 125 130

cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547
Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu
                        135 140 145

gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595
Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met
                        150 155 160 165

gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg 643
Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met
                        170 175 180

gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc 691
Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr
                        185 190 195

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cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgtttttagcg 789
 His Gly Ile Val Pro Asp Met Lys Lys Leu
 215 220

aaa 792

<213> Corynebacterium glutamicum

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu
210 215 220

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<222> (101) .. (703)  
<223> RXC01622
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gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163
Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly
10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211
Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg
25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259
Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val
 40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307
Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu
55 60 65

tgg	gtg	gac	ctc	acc	tcg	aag	cca	cag	gca	ctg	tac	atc	ggt	ggg	ccg	355
Trp	Val	Asp	Leu	Thr	Ser	Lys	Pro	Gln	Ala	Leu	Tyr	Ile	Gly	Gly	Pro	
70					75					80					85	

ttg	agc	cag	cag	gct	gtg	gtt	ggt	ttg	ggc	gtg	acc	aag	ccg	ggc	gtg	403
Leu	Ser	Gln	Gln	Ala	Val	Val	Gly	Leu	Gly	Val	Thr	Lys	Pro	Gly	Val	
				90					95					100		

gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451
Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val
105 110 115

cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu
 120 125 130

ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547
Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu
135 140 145

aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595
Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro
150 155 160 165

tgc	gac	att	atc	gcg	ccg	ggc	cgc	gtc	gat	att	tgg	ggc	gac	gtg	atg	643
Ser	Asp	Ile	Ile	Ala	Pro	Gly	Arg	Val	Asp	Ile	Trp	Gly	Asp	Val	Met	
				170					175					180		

cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691
 Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp
 185 190 195

cct tca gat aat tagatgagtt ccgaaaattt aaa 726
 Pro Ser Asp Asn
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<210> 1132

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 1132

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Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser
 20 25 30

Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala
 35 40 45

Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala
 50 55 60

Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu
 65 70 75 80

Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val
 85 90 95

Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu
 100 105 110

Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val
 115 120 125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp
 130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val
 145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile
 165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser
 180 185 190

Thr Phe Pro Ser Asp Pro Ser Asp Asn
 195 200

<210> 1133

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

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cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
Val Ser Lys Ile Ser
1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
10 15 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
40 45 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
55 60 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tgc act cgt att ttg gat cgc 403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
90 95 100

att gat ctg aac act ctg cca ggt tgc acg aat gcg gaa cga acg att 451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat 499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr
120 125 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa 547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu
135 140 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu
150 155 160 165

aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt 643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe
170 175 180

gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat 691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn
185 190 195

gag tgc cag tgc atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt 739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly

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200						205						210						
cct	tcg	ccg	gca	att	tct	cct	ggg	gtg	gtc	aat	cag	ctg	tcc	acg	gat			787
Pro	Ser	Pro	Ala	Ile	Ser	Pro	Gly	Val	Val	Asn	Gln	Leu	Ser	Thr	Asp			
	215						220				225							
gcg	tcg	ttc	gtg	ggg	ttc	aat	gat	ggg	gag	tat	cag	ttc	act	ggg	ttg			835
Ala	Ser	Phe	Val	Gly	Phe	Asn	Asp	Gly	Glu	Tyr	Gln	Phe	Thr	Gly	Leu			
	230				235					240					245			
gga	aat	ttg	gat	gat	gat	gcg	cgt	ttg	cgt	ttc	gcc	gcc	cag	gcc	gtg			883
Gly	Asn	Leu	Asp	Asp	Asp	Ala	Arg	Leu	Arg	Phe	Ala	Ala	Gln	Ala	Val			
				250					255					260				
tgg	acg	ttg	gcg	cat	gct	gat	gtc	gca	ggc	ccc	tac	act	ttg	gtc	gct			931
Trp	Thr	Leu	Ala	His	Ala	Asp	Val	Ala	Gly	Pro	Tyr	Thr	Leu	Val	Ala			
			265					270					275					
gac	ggc	gcg	ccg	ttg	ctg	tcg	gag	ttc	cca	acg	ctc	acc	acc	gat	gac			979
Asp	Gly	Ala	Pro	Leu	Leu	Ser	Glu	Phe	Pro	Thr	Leu	Thr	Thr	Asp	Asp			
		280					285					290						
ctc	gcc	gaa	tac	aac	cca	gag	gct	tac	acc	aac	acg	gtg	tcc	acg	ttg			1027
Leu	Ala	Glu	Tyr	Asn	Pro	Glu	Ala	Tyr	Thr	Asn	Thr	Val	Ser	Thr	Leu			
		295				300					305							
ttt	gcg	ttg	cag	gat	gga	tcg	ttg	tcg	agg	gtc	agt	tcc	ggc	aat	gtg			1075
Phe	Ala	Leu	Gln	Asp	Gly	Ser	Leu	Ser	Arg	Val	Ser	Ser	Gly	Asn	Val			
	310				315					320					325			
agt	cca	cta	cag	ggc	att	tgg	agc	ggg	gga	gat	atc	gat	tct	gca	gcg			1123
Ser	Pro	Leu	Gln	Gly	Ile	Trp	Ser	Gly	Gly	Asp	Ile	Asp	Ser	Ala	Ala			
				330					335					340				
att	tcc	tcc	tcc	gcc	aat	gtg	gtg	gca	gcg	gta	cgc	cac	gaa	aac	aac			1171
Ile	Ser	Ser	Ser	Ala	Asn	Val	Val	Ala	Ala	Val	Arg	His	Glu	Asn	Asn			
				345				350					355					
gag	gca	gtg	ctt	act	gtt	ggc	tcc	atg	gaa	ggc	gtg	act	tca	gat	gcg			1219
Glu	Ala	Val	Leu	Thr	Val	Gly	Ser	Met	Glu	Gly	Val	Thr	Ser	Asp	Ala			
		360					365					370						
ttg	agg	agt	gaa	acg	atc	act	cgt	ccc	acc	ttt	gaa	tac	gcg	tcg	agt			1267
Leu	Arg	Ser	Glu	Thr	Ile	Thr	Arg	Pro	Thr	Phe	Glu	Tyr	Ala	Ser	Ser			
	375					380					385							
ggg	ttg	tgg	gct	gtg	gtg	gat	ggg	gag	acg	cct	gtc	cga	gtc	gca	cga			1315
Gly	Leu	Trp	Ala	Val	Val	Asp	Gly	Glu	Thr	Pro	Val	Arg	Val	Ala	Arg			
	390				395					400					405			
tcg	gca	aca	acc	ggg	gag	ctc	gtc	cag	acg	gag	gcg	gag	att	gtg	ctg			1363
Ser	Ala	Thr	Thr	Gly	Glu	Leu	Val	Gln	Thr	Glu	Ala	Glu	Ile	Val	Leu			
				410				415						420				
cca	agg	gat	gtg	acg	ggg	ccg	atc	tct	gaa	ttc	caa	ctg	tca	cga	act			1411
Pro	Arg	Asp	Val	Thr	Gly	Pro	Ile	Ser	Glu	Phe	Gln	Leu	Ser	Arg	Thr			
				425				430					435					
ggg	gtc	cgg	gcc	gcc	atg	atc	att	gaa	ggc	aag	gtg	tac	gtg	ggc	gtc			1459
Gly	Val	Arg	Ala	Ala	Met	Ile	Ile	Glu	Gly	Lys	Val	Tyr	Val	Gly	Val			
		440					445					450						

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag 1507
 Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
 455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tgc atc aac tgg cgc cca 1555
 Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
 470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg 1603
 Asp Gly Ile Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
 490 495 500

cgc gtc gag cag gac gga tgc gcg att tgc tgc atg ccg agc ggg aat 1651
 Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
 505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac 1699
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
 520 525 530

gtc act gat tgc cat gcg atg ctt cag ctg ccg act gcc gat aat gat 1747
 Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
 535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg 1795
 Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
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gtt gcg tac tgatggagct gttcttcccg cgc 1827
 Val Ala Tyr

<210> 1134

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 1134

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 20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
 35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
 50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
 65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
 85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
 100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
 115 120 125
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
 130 135 140
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
 145 150 155 160
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
 165 170 175
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
 180 185 190
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
 195 200 205
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys

435					440					445					
Val	Tyr	Val	Gly	Val	Val	Thr	Arg	Pro	Gly	Pro	Gly	Glu	Arg	Arg	Val
450						455					460				
Thr	Asn	Ile	Thr	Glu	Val	Ala	Pro	Ser	Leu	Gly	Glu	Ala	Ala	Leu	Ser
465					470					475					480
Ile	Asn	Trp	Arg	Pro	Asp	Gly	Ile	Leu	Leu	Val	Gly	Thr	Ser	Ile	Pro
				485					490					495	
Glu	Thr	Pro	Leu	Trp	Arg	Val	Glu	Gln	Asp	Gly	Ser	Ala	Ile	Ser	Ser
			500					505					510		
Met	Pro	Ser	Gly	Asn	Leu	Ser	Ala	Pro	Val	Val	Ala	Val	Ala	Ser	Ser
		515					520					525			
Ala	Thr	Thr	Val	Tyr	Val	Thr	Asp	Ser	His	Ala	Met	Leu	Gln	Leu	Pro
	530					535					540				
Thr	Ala	Asp	Asn	Asp	Ile	Trp	Arg	Glu	Val	Pro	Gly	Leu	Leu	Gly	Thr
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Arg	Ala	Ala	Pro	Val	Val	Ala	Tyr								
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<210> 1135

<211> 555

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(532)

<223> RXC01709

<400> 1135

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gaaattaggt	gtcgatgcag	caatacggaa	ctttgccaat	gtg	ttt	gaa	caa	gct	115
				Val	Phe	Glu	Gln	Ala	
				1				5	

ctc	ggg	ctc	acc	acc	ctt	gca	caa	aca	gct	gga	gcg	ggc	gca	gcg	ggg	163
Leu	Gly	Leu	Thr	Thr	Leu	Ala	Gln	Thr	Ala	Gly	Ala	Gly	Ala	Ala	Gly	
			10					15					20			

ggc	ttg	ggt	ttc	atg	gca	atg	gcg	ttg	ttg	tct	gca	ggg	atg	cgc	tcc	211
Gly	Leu	Gly	Phe	Met	Ala	Met	Ala	Leu	Leu	Ser	Ala	Gly	Met	Arg	Ser	
			25					30					35			

ggc	gtg	gac	atg	att	ctt	aat	gaa	acc	ggg	ggt	gaa	aag	atg	ctt	gca	259
Gly	Val	Asp	Met	Ile	Leu	Asn	Glu	Thr	Gly	Gly	Glu	Lys	Met	Leu	Ala	
		40					45					50				

cag	gca	gat	tta	gtc	atc	act	gga	gaa	gga	cgc	att	gat	gca	cag	acc	307
Gln	Ala	Asp	Leu	Val	Ile	Thr	Gly	Glu	Gly	Arg	Ile	Asp	Ala	Gln	Thr	
	55					60					65					

ctc	agc	ggg	aaa	gct	cct	act	gga	atc	gcc	aaa	cgg	gca	cgt	gcg	aaa	355
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala Arg Ala Lys
 70 75 80 85
 gga att cca gta ctg gcg gtt tgt ggg cag agc cta ttg ggt cca gca 403
 Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu Gly Pro Ala
 90 95 100
 atc tca aat gag cta ttt gaa gac atc tac agc ttt acc gat ttc gaa 451
 Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr Asp Phe Glu
 105 110 115
 tct gac atc aat gaa tgc att cga aac ccg ctc cca att ttg gaa ggt 499
 Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile Leu Glu Gly
 120 125 130
 atc ggt ttt aac atc gcc aaa cat cat ctg agt tagcgatatt tcagcaaacc 552
 Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
 135 140
 gat 555

<210> 1136
 <211> 144
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1136
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 Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser
 20 25 30
 Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly
 35 40 45
 Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg
 50 55 60
 Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys
 65 70 75 80
 Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser
 85 90 95
 Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser
 100 105 110
 Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu
 115 120 125
 Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
 130 135 140

<210> 1137
 <211> 898

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(898)

<223> RXC02207

<400> 1137

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ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115
Met Arg Arg Arg Ser
1 5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163
Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala
10 15 20

ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg 211
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met
25 30 35

ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc 259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly
40 45 50

caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt 307
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly
55 60 65

gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc 355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val
70 75 80 85

tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa 403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln
90 95 100

tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc 451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala
105 110 115

gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg 499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu
120 125 130

cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat 547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp
135 140 145

cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc 595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg
150 155 160 165

gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag 643
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln
170 175 180

ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc 691
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr

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185							190					195					
tgg	aac	gaa	aac	acc	acg	att	caa	gat	gtg	gac	tac	ccc	aac	gac	cgt	739	
Trp	Asn	Glu	Asn	Thr	Thr	Ile	Gln	Asp	Val	Asp	Tyr	Pro	Asn	Asp	Arg		
		200					205					210					
gaa	ggc	gcg	acc	ctt	cgc	gtg	gga	ctc	ggc	gtt	ggg	caa	atg	gct	ggg	787	
Glu	Gly	Ala	Thr	Leu	Arg	Val	Gly	Leu	Gly	Val	Gly	Gln	Met	Ala	Gly		
	215					220				225							
ggc	gaa	gac	ggc	ctg	ctg	gtg	gtc	tct	gat	gaa	atg	ggg	ggc	caa	att	835	
Gly	Glu	Asp	Gly	Leu	Leu	Val	Val	Ser	Asp	Glu	Met	Gly	Gly	Gln	Ile		
230				235						240					245		
gcc	atc	tac	aac	gct	gat	gat	gtc	atc	cga	ctt	caa	aat	gac	cgc	ccc	883	
Ala	Ile	Tyr	Asn	Ala	Asp	Asp	Val	Ile	Arg	Leu	Gln	Asn	Asp	Arg	Pro		
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cac	cga	cga	gga	acc												898	
His	Arg	Arg	Gly	Thr													
			265														

<210> 1138

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 1138

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Leu	Ala	Ser	Thr	Ala	Leu	Leu	Leu	Ser	Ala	Cys	Thr	Gln	Gly	Val	Thr	
			20					25					30			
Asp	Ser	Pro	Asp	Met	Gly	Lys	Ala	Thr	Pro	Ala	Val	Ser	Pro	Ala	Ala	
		35					40					45				
Ser	Asn	Pro	Asp	Gly	Gln	Val	Ile	Glu	Phe	Gly	Asn	Ile	Thr	Asp	Met	
	50					55					60					
Glu	Val	Thr	Asp	Gly	Asp	Ile	Leu	Gly	Val	Arg	Thr	Glu	Asp	Ala	Leu	
65					70				75						80	
Ala	Ile	Gly	Thr	Val	Ser	Asp	Phe	Glu	Ala	Gly	Ser	Gln	Val	Glu	Leu	
				85				90						95		
Asp	Val	Asp	Lys	Gln	Cys	Gly	Asp	Leu	Thr	Ala	Thr	Gly	Gly	Thr	Phe	
		100						105					110			
Val	Leu	Pro	Cys	Ala	Asp	Gly	Val	Tyr	Leu	Ile	Asp	Ala	Lys	Asp	Pro	
		115					120					125				
Asp	Leu	Asp	Glu	Leu	Arg	Ala	Thr	Asp	Lys	Pro	Val	Thr	Val	Ala	Ala	
	130					135					140					
Leu	Thr	Ser	Asp	Asp	Gln	Leu	Leu	Val	Gly	Asn	Gly	Glu	Asp	Glu	Glu	
145					150					155					160	
Leu	Thr	Ile	Tyr	Arg	Glu	Gly	Glu	Glu	Pro	Glu	Thr	Phe	Thr	Val	Ala	
				165				170						175		

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp
 180 185 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp
 195 200 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val
 210 215 220

Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu
 225 230 235 240

Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu
 245 250 255

Gln Asn Asp Arg Pro His Arg Arg Gly Thr
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<210> 1139

<211> 891

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(868)

<223> RXA00347

<400> 1139

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aaagtgccag gggttctgtg ggatccgtac actgggttccc atg act ttg act att 115
 Met Thr Leu Thr Ile
 1 5

gag gaa atc gcc aag acc aaa aag ctt ttg gtt gtg tcc gat ttt gat 163
 Glu Glu Ile Ala Lys Thr Lys Lys Leu Leu Val Val Ser Asp Phe Asp
 10 15 20

gga acc atc gca gga ttt agc aag gac gct tac aac gtt cct atc aac 211
 Gly Thr Ile Ala Gly Phe Ser Lys Asp Ala Tyr Asn Val Pro Ile Asn
 25 30 35

cag aaa tcc ctc aag gcg gta aaa gac ctc tcc caa caa gca gac act 259
 Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser Gln Gln Ala Asp Thr
 40 45 50

gat gtt gtc att ttg tcg gga cgt cac ctg gag gga ttg aag acg gtt 307
 Asp Val Val Ile Leu Ser Gly Arg His Leu Glu Gly Leu Lys Thr Val
 55 60 65

ctt gat ctt ggt cag tac gac atc acc atg gtg ggt tca cac ggt tct 355
 Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val Gly Ser His Gly Ser
 70 75 80 85

gag gat tcc tcc cgc ccg cgt acc ctc act cct gaa gag gta gct cgc 403
 Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro Glu Glu Val Ala Arg
 90 95 100

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ctc gcc aag att gaa gca gat ctg gaa aag atc gtc gac ggc atc gaa 451
Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile Val Asp Gly Ile Glu
      105                      110                      115

ggc gca ttc gtg gag atc aag cct ttc cac cgc gtg ctg cac ttc atc 499
Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg Val Leu His Phe Ile
      120                      125                      130

cgt gtt tcc gac aag gac aaa gtc caa gga atc ctc gcc caa gca gca 547
Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile Leu Ala Gln Ala Ala
      135                      140                      145

cac gta gac tct tcc ggc ctg aag gtt act aac ggc aag agc atc atc 595
His Val Asp Ser Ser Gly Leu Lys Val Thr Asn Gly Lys Ser Ile Ile
      150                      155                      160                      165

gaa tac tcc atc agc tcc acc acc aag ggc acc tgg ctg aag gaa tac 643
Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr Trp Leu Lys Glu Tyr
      170                      175                      180

gtt gac cgc acc gag ccc act ggt gtg att ttc ctc ggc gat gac acc 691
Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe Leu Gly Asp Asp Thr
      185                      190                      195

acc gat gag cac ggt ttc aaa gct tta gaa aac gat gat cgt gcc cta 739
Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn Asp Asp Arg Ala Leu
      200                      205                      210

acc gtc aag gtt ggc gaa gga gac act gca gcc aaa acc cgc gtc gac 787
Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala Lys Thr Arg Val Asp
      215                      220                      225

gat gtt gat aat gtg gga att ttc cta gag aaa ctc gcc tac cac cgc 835
Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys Leu Ala Tyr His Arg
      230                      235                      240                      245

atg cag tat gcg gaa agc gtg cga ttg ggg att taagagagcc taaacgcacg 888
Met Gln Tyr Ala Glu Ser Val Arg Leu Gly Ile
      250                      255

aaa 891

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<210> 1140

<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 1140

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Asn Val Pro Ile Asn Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser
      35                      40                      45

Gln Gln Ala Asp Thr Asp Val Val Ile Leu Ser Gly Arg His Leu Glu
      50                      55                      60

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Gly Leu Lys Thr Val Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val
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 Gly Ser His Gly Ser Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro
 85 90 95
 Glu Glu Val Ala Arg Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile
 100 105 110
 Val Asp Gly Ile Glu Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg
 115 120 125
 Val Leu His Phe Ile Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile
 130 135 140
 Leu Ala Gln Ala Ala His Val Asp Ser Ser Gly Leu Lys Val Thr Asn
 145 150 155 160
 Gly Lys Ser Ile Ile Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr
 165 170 175
 Trp Leu Lys Glu Tyr Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe
 180 185 190
 Leu Gly Asp Asp Thr Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn
 195 200 205
 Asp Asp Arg Ala Leu Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala
 210 215 220
 Lys Thr Arg Val Asp Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys
 225 230 235 240
 Leu Ala Tyr His Arg Met Gln Tyr Ala Glu Ser Val Arg Leu Gly Ile
 245 250 255

<210> 1141

<211> 2556

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2533)

<223> RXN01239

<400> 1141

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gtaccgcacg attttgccta acttttaagg gtgtttcatc atg gca cgt cca att 115
 Met Ala Arg Pro Ile
 1 5

tcc gca acg tac agg ctt caa atg cga gga cct caa gca gat agc gcc 163
 Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala
 10 15 20

ggg cgt tca ttt ggt ttt gcg cag gcc aaa gcc cag ctt ccc tat ctg	211
Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu	
25 30 35	
aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc	259
Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala	
40 45 50	
atg cca gat tcc aat cat ggc tac gat gtc att gat ccc acc acc atc	307
Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile	
55 60 65	
aat gaa gag ctc ggt ggc atg gag ggt ctt cga gat ctt gcc gca gct	355
Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala	
70 75 80 85	
aca cac gag ttg ggc atg ggc atc atc att gat att gtt ccc aac cat	403
Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His	
90 95 100	
tta ggt gtt gcc gtt cca cat ttg aat cct tgg tgg tgg gat gtt cta	451
Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu	
105 110 115	
aaa aac ggc aaa gat tcc gct ttt gag ttc tat ttc gat att gac tgg	499
Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp	
120 125 130	
cac gaa gac aac ggt tct ggt ggc aag ctg ggc atg ccg att ctg ggt	547
His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly	
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 Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp
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 Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp
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 Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly
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Ala	Arg	Ala	Met	Arg	Arg	Asp	Asn	Phe	Ser	Thr	Ala	Gly	Thr	Asn	Val		
		360					365					370					
acc	gaa	gac	aaa	ctt	agc	gaa	acc	atc	atc	gaa	tta	gtc	gcc	gcc	atg	1267	
Thr	Glu	Asp	Lys	Leu	Ser	Glu	Thr	Ile	Ile	Glu	Leu	Val	Ala	Ala	Met		
	375					380					385						
ccc	gtc	tac	cgc	gcc	gac	tac	atc	tcc	ctc	tca	cgc	acc	acc	gcc	acc	1315	
Pro	Val	Tyr	Arg	Ala	Asp	Tyr	Ile	Ser	Leu	Ser	Arg	Thr	Thr	Ala	Thr		
390					395					400					405		
gtc	atc	gcg	gag	atg	tcc	aaa	cgc	ttc	ccc	tcc	cgg	cgt	gac	gca	ctc	1363	
Val	Ile	Ala	Glu	Met	Ser	Lys	Arg	Phe	Pro	Ser	Arg	Arg	Asp	Ala	Leu		
				410					415					420			
gac	ctc	atc	gcg	gcc	gcc	cta	ctt	ggc	aat	ggc	gag	gcc	aaa	atc	cgc	1411	
Asp	Leu	Ile	Ala	Ala	Ala	Leu	Leu	Gly	Asn	Gly	Glu	Ala	Lys	Ile	Arg		
			425					430					435				
ttc	gct	caa	gtc	tgc	ggc	gcc	gtc	atg	gct	aaa	ggt	gtg	gaa	gac	acc	1459	
Phe	Ala	Gln	Val	Cys	Gly	Ala	Val	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr		

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acc	ttc	tac	cgc	gca	tct	agg	ctc	gtt	gca	ttg	caa	gaa	gtc	ggt	ggc	1507	
Thr	Phe	Tyr	Arg	Ala	Ser	Arg	Leu	Val	Ala	Leu	Gln	Glu	Val	Gly	Gly		
455						460					465						
gcg	ccg	ggg	aga	ttc	ggc	gtc	tcc	gct	gca	gaa	ttc	cac	ttg	ctg	cag	1555	
Ala	Pro	Gly	Arg	Phe	Gly	Val	Ser	Ala	Ala	Glu	Phe	His	Leu	Leu	Gln		
470						475					480					485	
gaa	gaa	cgc	agc	ctg	ctg	tgg	cca	cgc	acc	atg	acc	acc	ttg	tcc	acg	1603	
Glu	Glu	Arg	Ser	Leu	Leu	Trp	Pro	Arg	Thr	Met	Thr	Thr	Leu	Ser	Thr		
490						495					500						
cat	gac	acc	aaa	cgt	ggc	gaa	gat	acc	cgc	gcc	cgc	atc	atc	tcc	ctg	1651	
His	Asp	Thr	Lys	Arg	Gly	Glu	Asp	Thr	Arg	Ala	Arg	Ile	Ile	Ser	Leu		
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tct	gaa	gtc	ccc	gat	atg	tac	tcc	gag	ctg	gtc	aat	cgt	gtt	ttc	gcg	1699	
Ser	Glu	Val	Pro	Asp	Met	Tyr	Ser	Glu	Leu	Val	Asn	Arg	Val	Phe	Ala		
520						525					530						
gtg	ctc	ccc	gcg	cca	gac	ggc	gca	acg	ggc	agt	ttc	ctc	cta	caa	aac	1747	
Val	Leu	Pro	Ala	Pro	Asp	Gly	Ala	Thr	Gly	Ser	Phe	Leu	Leu	Gln	Asn		
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ctg	ctg	ggc	gta	tgg	ccc	gcc	gac	ggc	gtg	atc	acc	gat	gcg	ctg	cgc	1795	
Leu	Leu	Gly	Val	Trp	Pro	Ala	Asp	Gly	Val	Ile	Thr	Asp	Ala	Leu	Arg		
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gat	cga	ttc	agg	gaa	tac	gcc	cta	aaa	gct	atc	cgc	gaa	gca	tcc	aca	1843	
Asp	Arg	Phe	Arg	Glu	Tyr	Ala	Leu	Lys	Ala	Ile	Arg	Glu	Ala	Ser	Thr		
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Lys	Thr	Thr	Trp	Val	Asp	Pro	Asn	Glu	Ser	Phe	Glu	Ala	Ala	Val	Cys		
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gat	tgg	gtg	gaa	gcg	ctt	ttc	gac	gga	ccc	tcc	acc	tca	cta	atc	acc	1939	
Asp	Trp	Val	Glu	Ala	Leu	Phe	Asp	Gly	Pro	Ser	Thr	Ser	Leu	Ile	Thr		
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gaa	ttt	gtc	tcc	cac	atc	aac	cgt	ggc	tct	gtg	caa	atc	tcc	tta	ggc	1987	
Glu	Phe	Val	Ser	His	Ile	Asn	Arg	Gly	Ser	Val	Gln	Ile	Ser	Leu	Gly		
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Arg	Lys	Leu	Leu	Gln	Met	Val	Gly	Ala	Gly	Ile	Pro	Asp	Thr	Tyr	Gln		
630						635					640					645	
gga	act	gag	ttt	tta	gaa	gac	tcc	ctg	gta	gat	ccc	gat	aac	cga	cgc	2083	
Gly	Thr	Glu	Phe	Leu	Glu	Asp	Ser	Leu	Val	Asp	Pro	Asp	Asn	Arg	Arg		
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Phe	Val	Asp	Tyr	Thr	Ala	Arg	Glu	Gln	Val	Leu	Glu	Arg	Leu	Gln	Thr		
665						670					675						
tgg	gat	tgg	acg	cag	gtt	aat	tcg	gta	gaa	gac	ttg	gtg	gat	aac	gcc	2179	
Trp	Asp	Trp	Thr	Gln	Val	Asn	Ser	Val	Glu	Asp	Leu	Val	Asp	Asn	Ala		
680						685					690						

gac atc gcc aaa atg gcc gtg gtc cat aaa tcc ctc gag ttg cgt gct 2227
 Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala
 695 700 705

gaa ttt cgt gca agc ttt gtt ggt gga gat cat cag gca gta ttt ggc 2275
 Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His Gln Ala Val Phe Gly
 710 715 720 725

gaa ggt cgc gca gaa tcc cac atc atg ggc atc gcc cgc ggt aca gac 2323
 Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp
 730 735 740

cga aac cac ctc aac atc att gct ctt gct acc cgt cga cca ctg atc 2371
 Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile
 745 750 755

ttg gaa gac cgt ggc gga tgg tat gac acc acc gtc acg ctt cct ggt 2419
 Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly
 760 765 770

gga caa tgg gaa gac agg ctc acc ggg caa cgc ttc agt ggt gtt gtc 2467
 Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val
 775 780 785

cca gcc acc gat ttg ttc tca cat cta ccc gta tct ttg ttg gtt tta 2515
 Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu
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<210> 1144

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<213> Corynebacterium glutamicum

<400> 1144

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Gln Leu Pro Tyr Leu Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser
 35 40 45

Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile
 50 55 60

Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg
 65 70 75 80

Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp
 85 90 95

Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp
 100 105 110

Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr
 115 120 125
 Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly
 130 135 140
 Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala
 145 150 155 160
 Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro
 165 170 175
 Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg
 180 185 190
 Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg
 195 200 205
 Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro
 210 215 220
 Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu
 225 230 235 240
 Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp
 245 250 255
 Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg
 260 265 270
 Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro
 275 280 285
 Arg Leu Ala Val Asp Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu
 290 295 300
 Asp Gly Val Phe Ile Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu
 305 310 315 320
 Ala Leu Thr His Ser Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser
 325 330 335
 Thr Glu Glu Ser Leu Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala
 340 345 350
 Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr
 355 360 365
 Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu
 370 375 380
 Leu Val Ala Ala Met Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser
 385 390 395 400
 Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser
 405 410 415
 Arg Arg Asp Ala Leu Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly
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 Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys

435					440					445					
Gly	Val	Glu	Asp	Thr	Thr	Phe	Tyr	Arg	Ala	Ser	Arg	Leu	Val	Ala	Leu
450					455					460					
Gln	Glu	Val	Gly	Gly	Ala	Pro	Gly	Arg	Phe	Gly	Val	Ser	Ala	Ala	Glu
465					470					475					480
Phe	His	Leu	Leu	Gln	Glu	Glu	Arg	Ser	Leu	Leu	Trp	Pro	Arg	Thr	Met
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Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Gly	Glu	Asp	Thr	Arg	Ala
			500					505					510		
Arg	Ile	Ile	Ser	Leu	Ser	Glu	Val	Pro	Asp	Met	Tyr	Ser	Glu	Leu	Val
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Asn	Arg	Val	Phe	Ala	Val	Leu	Pro	Ala	Pro	Asp	Gly	Ala	Thr	Gly	Ser
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Phe	Leu	Leu	Gln	Asn	Leu	Leu	Gly	Val	Trp	Pro	Ala	Asp	Gly	Val	Ile
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Thr	Asp	Ala	Leu	Arg	Asp	Arg	Phe	Arg	Glu	Tyr	Ala	Leu	Lys	Ala	Ile
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Arg	Glu	Ala	Ser	Thr	Lys	Thr	Thr	Trp	Val	Asp	Pro	Asn	Glu	Ser	Phe
			580					585					590		
Glu	Ala	Ala	Val	Cys	Asp	Trp	Val	Glu	Ala	Leu	Phe	Asp	Gly	Pro	Ser
			595					600					605		
Thr	Ser	Leu	Ile	Thr	Glu	Phe	Val	Ser	His	Ile	Asn	Arg	Gly	Ser	Val
			610					615					620		
Gln	Ile	Ser	Leu	Gly	Arg	Lys	Leu	Leu	Gln	Met	Val	Gly	Ala	Gly	Ile
625					630					635					640
Pro	Asp	Thr	Tyr	Gln	Gly	Thr	Glu	Phe	Leu	Glu	Asp	Ser	Leu	Val	Asp
				645					650					655	
Pro	Asp	Asn	Arg	Arg	Phe	Val	Asp	Tyr	Thr	Ala	Arg	Glu	Gln	Val	Leu
			660					665					670		
Glu	Arg	Leu	Gln	Thr	Trp	Asp	Trp	Thr	Gln	Val	Asn	Ser	Val	Glu	Asp
			675					680					685		
Leu	Val	Asp	Asn	Ala	Asp	Ile	Ala	Lys	Met	Ala	Val	Val	His	Lys	Ser
			690					695					700		
Leu	Glu	Leu	Arg	Ala	Glu	Phe	Arg	Ala	Ser	Phe	Val	Gly	Gly	Asp	His
705					710					715					720
Gln	Ala	Val	Phe	Gly	Glu	Gly	Arg	Ala	Glu	Ser	His	Ile	Met	Gly	Ile
				725					730					735	
Ala	Arg	Gly	Thr	Asp	Arg	Asn	His	Leu	Asn	Ile	Ile	Ala	Leu	Ala	Thr
			740					745					750		
Arg	Arg	Pro	Leu	Ile	Leu	Glu	Asp	Arg	Gly	Gly	Trp	Tyr	Asp	Thr	Thr
			755					760					765		

Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg
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Phe Ser Gly Val Val Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val
785 790 795 800

Ser Leu Leu Val Leu Val Pro Asp Ser Glu Phe
805 810

<210> 1145

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1930)

<223> RXA02645

<400> 1145

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Met Leu Lys Asp Leu
1 5

acc ggc ctg agg gag ttg gta ttg cgt gag atg tgc cat agc atc tca 163
Thr Gly Leu Arg Glu Leu Val Leu Arg Glu Met Cys His Ser Ile Ser
10 15 20

cat ctt agc tcg cca acc ggc agc att ttc act agc ctg gtg gcc atg 211
His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr Ser Leu Val Ala Met
25 30 35

ttg acc tcg caa agc ttt tca gtg tgg gct cca ctt ccc cac gat gta 259
Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro Leu Pro His Asp Val
40 45 50

cat ctg atc ctc aac ggc gaa acc ctc ccc atg cac aaa acg gag ggc 307
His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met His Lys Thr Glu Gly
55 60 65

agc tgg tgg cgc gcc gag atc gcg ccc aag gcc ggc gat cgt tac ggt 355
Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala Gly Asp Arg Tyr Gly
70 75 80 85

ttt tcg ctt ttc gac ggc tcc tcc tgg tca aaa acc ctc ccc gat ccc 403
Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys Thr Leu Pro Asp Pro
90 95 100

cgc tcc aca tct caa cca gac ggg gtt cat ggt tta agt gaa gtc tcc 451
Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly Leu Ser Glu Val Ser
105 110 115

gat gat tcc tat ctg tgg ggt gac cag cag tgg act ggc cga att ctc 499
Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp Thr Gly Arg Ile Leu
120 125 130

cct ggc tcg gtg tta tat gag ctg cat gtg ggc acc ttt agt gaa gat 547

Pro	Gly	Ser	Val	Leu	Tyr	Glu	Leu	His	Val	Gly	Thr	Phe	Ser	Glu	Asp		
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Gly	Val	Thr	Ala	Ile	Glu	Leu	Leu	Pro	Val	Gln	Pro	Phe	Gly	Gly	Asn	180	
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cgc	aat	tgg	ggc	tac	gac	ggg	gtg	ctg	tgg	cac	gcc	gtc	cat	gca	ggc	691	
Arg	Asn	Trp	Gly	Tyr	Asp	Gly	Val	Leu	Trp	His	Ala	Val	His	Ala	Gly	195	
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tac	ggc	ggg	ccg	gcg	ggc	ttg	aaa	aag	ctt	atc	gac	gcc	tcc	cac	cag	739	
Tyr	Gly	Gly	Pro	Ala	Gly	Leu	Lys	Lys	Leu	Ile	Asp	Ala	Ser	His	Gln	210	
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gcc	ggc	atc	gcc	gtc	tac	tta	gac	gtc	gtg	tac	aac	cac	ttc	ggc	ccc	787	
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230					235					240							
acc	ggc	tgg	ggc	gac	gtg	gtc	aac	atc	aac	ggc	cat	gat	tca	gat	gaa	883	
Thr	Gly	Trp	Gly	Asp	Val	Val	Asn	Ile	Asn	Gly	His	Asp	Ser	Asp	Glu	260	
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gtc	cgc	aat	tat	att	ctc	gac	gcc	gca	cgc	cag	tgg	ttc	gaa	gat	ttt	931	
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cac	gtt	gat	ggg	ctc	cgc	ctc	gat	gcg	gtg	cat	tct	ctc	gat	gat	cgc	979	
His	Val	Asp	Gly	Leu	Arg	Leu	Asp	Ala	Val	His	Ser	Leu	Asp	Asp	Arg	290	
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Asp	Ala	Gln	Trp	Val	Asp	Asp	Ile	His	His	Ala	Leu	His	Ala	Leu	Val	355	
			345					350									
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Ser	Gly	Glu	Arg	Asn	Gly	Tyr	Tyr	Ser	Asp	Phe	Gly	Ser	Val	Asp	Thr	370	
		360				365											
tta	gcc	aaa	acc	ctg	cgt	gaa	gta	ttt	gaa	cac	acc	gga	aac	tac	tcc	1267	
Leu	Ala	Lys	Thr	Leu	Arg	Glu	Val	Phe	Glu	His	Thr	Gly	Asn	Tyr	Ser		

375	380	385	
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cct gcc tcg cgc ttt gtc acc tac acc acc acc cat gat cag acc ggc Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr His Asp Gln Thr Gly 410 415 420			1363
aac cgc gca atc ggc gac cgt cct tcc acg act ctc acc ccg gaa cag Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr Leu Thr Pro Glu Gln 425 430 435			1411
cag gtg ttg aag gca gcc att atc tac agc tcg ccg tat acc ccg atg Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser Pro Tyr Thr Pro Met 440 445 450			1459
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aaa cgg gaa ttc gca cgc ctt ggc tgg aac gcc gac gac atc ccc tcc Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala Asp Asp Ile Pro Ser 490 495 500			1603
ccc gag ctg gaa tcc acc ttc acc tcc tcc aaa ctc gat tgg gag ttc Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys Leu Asp Trp Glu Phe 505 510 515			1651
act gcg gag cag cgc cgc atc aac gac gct tac aag cag ctg ttg cac Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr Lys Gln Leu Leu His 520 525 530			1699
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acc ctt cag ccg tgg ggc ttt gcg atc ctg acc cga aac tagaaaaagg Thr Leu Gln Pro Trp Gly Phe Ala Ile Leu Thr Arg Asn 600 605 610			1940
ccacctcgat tga			1953

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<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 1146

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Ser Leu Val Ala Met Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro
 35 40 45

Leu Pro His Asp Val His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met
 50 55 60

His Lys Thr Glu Gly Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala
 65 70 75 80

Gly Asp Arg Tyr Gly Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys
 85 90 95

Thr Leu Pro Asp Pro Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly
 100 105 110

Leu Ser Glu Val Ser Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp
 115 120 125

Thr Gly Arg Ile Leu Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly
 130 135 140

Thr Phe Ser Glu Asp Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro
 145 150 155 160

Tyr Leu Arg Asp Leu Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln
 165 170 175

Pro Phe Gly Gly Asn Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His
 180 185 190

Ala Val His Ala Gly Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile
 195 200 205

Asp Ala Ser His Gln Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr
 210 215 220

Asn His Phe Gly Pro Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr
 225 230 235 240

Thr Ser Gly Gly Ser Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly
 245 250 255

His Asp Ser Asp Glu Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln
 260 265 270

Trp Phe Glu Asp Phe His Val Asp Gly Leu Arg Leu Asp Ala Val His
 275 280 285

Ser Leu Asp Asp Arg Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met

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Asn	Gly	Arg	Gly	Arg	Ile	Leu	Ala	Asn	Phe	Ser	Asp	Asp	Thr	Ile	Thr
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Val	Pro	Leu	Gly	Gly	Glu	Leu	Ile	Tyr	Ser	Phe	Thr	Ser	Pro	Thr	Val
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Arg Lys Thr Gly Ala Ser Leu Ala Ala Thr Thr Leu Leu Ala Ala Ile
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Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser Asp Ser Thr Asp Ser
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Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile Trp Thr Ala Asp Phe
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Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser Ala Thr Tyr Asn Gly
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Ile	Asp	Arg	Trp	Asn	Glu	Ala	His	Pro	Asp	Glu	Gln	Val	Thr	Leu	Asn
	65				70					75					80
Glu	Leu	Ala	Gly	Glu	Ala	Asp	Ala	Gln	Arg	Glu	Thr	Leu	Val	Gln	Ser
				85				90						95	
Leu	Gln	Ala	Gly	Asn	Ser	Asp	Tyr	Asp	Val	Met	Ala	Leu	Asp	Val	Ile
			100					105					110		
Trp	Thr	Ala	Asp	Phe	Ala	Ala	Asn	Gln	Trp	Leu	Ala	Pro	Leu	Glu	Gly
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Ala	Thr	Tyr	Asn	Gly	Thr	Leu	Tyr	Ala	Leu	Pro	Gln	Asn	Thr	Asn	Gly
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Gln	Leu	Leu	Phe	Arg	Asn	Thr	Glu	Ile	Ile	Pro	Glu	Ala	Pro	Ala	Asn
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Trp	Ala	Asp	Leu	Val	Glu	Ser	Cys	Thr	Leu	Ala	Glu	Glu	Ala	Gly	Val
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 195 200 205
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 Met Asn Arg Ala Arg
 1 5
 atc gcg acc ata ggc gtt ctt ccg ctt got tta ctg ctg gcg tcc tgt 163
 Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu Leu Leu Ala Ser Cys
 10 15 20
 ggt tca gac acc gtg gaa atg aca gat tcc acc tgg ttg gtg acc aat 211
 Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr Trp Leu Val Thr Asn
 25 30 35
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 Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile Ser Asn Leu Val Ile
 40 45 50
 tcc cag ccc agc tta gat ttt ggc aat tct tcc ctg tct ggt ttc act 307
 Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser Leu Ser Gly Phe Thr
 55 60 65
 ggc tgt gtg cct ttt acg ggg cgt gcg gaa ttc ttc caa aat ggt gag 355
 Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe Phe Gln Asn Gly Glu
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 Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr Leu Ser Ser Leu Asp
 90 95 100
 ttc gat aaa ctt ccc gat gat tgc caa gga caa gaa ctc aaa gtt cat 451
 Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln Glu Leu Lys Val His
 105 110 115
 aac gag ctg gtt gat ctt ctg cct ggt tct ttt gaa atc tcc agg act 499
 Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe Glu Ile Ser Arg Thr
 120 125 130

tct ggt tca gaa atc ttg ctg act agc gat gtc gat gaa ctc gat cgg 547
 Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val Asp Glu Leu Asp Arg
 135 140 145

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 35 40 45

Ser Asn Leu Val Ile Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser
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Leu Ser Gly Phe Thr Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe
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Phe Gln Asn Gly Glu Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr
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Leu Ser Ser Leu Asp Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln
 100 105 110

Glu Leu Lys Val His Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe
 115 120 125

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ccg Pro	cca Pro	tcg Ser	cca Pro	cta Leu	gcc Ala	ccg Pro	att Ile	gat Asp	ctc Leu	act Thr	gac Asp	cat His	agt Ser	caa Gln	gtg Val	211
gcc Ala	ggt Gly	gtg Val	atg Met	aat Asn	ttg Leu	gct Ala	gcg Ala	aga Arg	att Ile	ggc Gly	gat Asp	att Ile	ttg Leu	ctt Leu	tct Ser	259
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Val	Gly	Cys	Tyr	Ala	Glu	Trp	Ser	Ser	Val	Ile	Ile	Ala	Gly	Leu	Thr	
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Tyr	Ala	Thr	Leu	Asn	Asp	Gln	Thr	Leu	Met	Gly	Phe	Thr	Asn	Ile	Ala	
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Glu	Trp	Ile	Ala	Arg	Arg	Leu	Arg	Arg	Pro	Pro	Arg	Phe	Asn	Pro	Tyr	
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cgt	gca	ttt	acc	aag	gcg	aat	gag	ttc	tcc	ttc	cag	gag	gaa	gct	gag	1507
Arg	Ala	Phe	Thr	Lys	Ala	Asn	Glu	Phe	Ser	Phe	Gln	Glu	Glu	Ala	Glu	

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Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln
 50 55 60

Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp
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Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg
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Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn
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 115 120 125

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Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser
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Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly
 195 200 205

Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu
 210 215 220

Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile
 225 230 235 240

Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly
245 250 255

Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu
260 265 270

Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu
275 280 285

Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala
290 295 300

Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr
305 310 315 320

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325 330 335

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340 345 350

Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala
355 360 365

Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro
370 375 380

Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala
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Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly
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Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala
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Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe
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<223> RXS03183

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 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe
 35 40 45
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 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro
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 cca gtt ctg gca tcc atc tac gat gat gag tcc ctt gtt gag cag tac 240
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr
 65 70 75 80
 cca tac ctg cca gca ctg aag gaa tcc ctg gaa aac gca gca cca cgc 288
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg
 85 90 95
 cca gtg tct cct ttc tac cca gcc atc tcc aag gca atc cag gac aac 336
 Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn
 100 105 110
 gcc tac gca gcg ctt aac ggc aac gtc gac gtt gac cag gca acc acc 384
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr
 115 120 125
 gat atg aag gca gcg atc gaa aac gct tcc agc tagttcggta atttagttca 437
 Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser
 130 135

ttc 440

<210> 1154

<211> 139

<212> PRT

<213> Corynebacterium glutamicum

<400> 1154

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 Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile
 20 25 30
 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe
 35 40 45
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro
 50 55 60
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr
 65 70 75 80
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg

85

90

95

Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn
 100 105 110
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr
 115 120 125
 Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser
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<210> 1155

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<213> Corynebacterium glutamicum

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 Met Ser Ile Gly Gln
 1 5
 cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac 163
 His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp
 10 15 20
 aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct 211
 Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly Glu Asn Thr Leu Ala
 25 30 35
 gta gtg cgc atc aac aat gcg ctg tat cag ttg ttg gtc aat gat gat 259
 Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu Leu Val Asn Asp Asp
 40 45 50
 ggc aaa gat gtt ctc aac gac cac gta gaa gag gtc ggt gcg agt ttc 307
 Gly Lys Asp Val Leu Asn Asp His Val Glu Glu Val Gly Ala Ser Phe
 55 60 65
 gga gca tgg act ggc agc tct gct ttt ccc att ggc cct ttc act cca 355
 Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile Gly Pro Phe Thr Pro
 70 75 80 85
 ctc ggc aca gaa caa tcc aat agc tct ttc atc acc gcc gac aat aaa 403
 Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile Thr Ala Asp Asn Lys
 90 95 100
 gcg atc gtg aaa tac ttc cgc aaa tta gaa tcc ggg caa aac ccc gat 451
 Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser Gly Gln Asn Pro Asp
 105 110 115
 gtg gag cta att tct aaa att tcc tcc tgc ccc aac atc gcg ccc atc 499
 Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro Asn Ile Ala Pro Ile
 120 125 130

ctg ggt ttt tcc tcc gct gag atc tcc ggg gct aac tac acc ctg gtc	547
Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala Asn Tyr Thr Leu Val	
135 140 145	
atg gcg cag cag tac gtt cca ggt ttg gat ggc tgg tca cac gcg ctg	595
Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly Trp Ser His Ala Leu	
150 155 160 165	
act act acc tct ggc agc ttt gca gag gat gca gaa aag atc ggc gaa	643
Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala Glu Lys Ile Gly Glu	
170 175 180	
gcc acc cgc aat gtt cac act gct ctt gca tcg gcc ttc cct act cgg	691
Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser Ala Phe Pro Thr Arg	
185 190 195	
gta gtt ccc gta gaa gca ctc gcc gat gcg ctc act acc cgc ctt aat	739
Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu Thr Thr Arg Leu Asn	
200 205 210	
gaa cta atc tcc caa gca ccc gaa atc gcc cgc ttc aaa gaa gca gcc	787
Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg Phe Lys Glu Ala Ala	
215 220 225	
atc gac ctc tac caa tcg ttg gaa ggc gaa gcc cac atc caa cgc atc	835
Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala His Ile Gln Arg Ile	
230 235 240 245	
cac ggt gac ctc cac ttg ggg cag ctc atc aaa acc ccc gaa cgc tac	883
His Gly Asp Leu His Leu Gly Gln Leu Ile Lys Thr Pro Glu Arg Tyr	
250 255 260	
atc ctc atc gat ttc gaa ggc gaa cct gcc cgc cca ctt aat caa cga	931
Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg Pro Leu Asn Gln Arg	
265 270 275	
cgc ctc ccc gac tct ccc ctg aaa gat ctc gcc ggc atc atc aga tcc	979
Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser	
280 285 290	
atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac	1027
Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn	
295 300 305	
gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa	1075
Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln	
310 315 320 325	
gaa ctc ctc aat gcc tac att ctg gac aag gcg ttg tac gag gtt gcc	1123
Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala	
330 335 340	
tat gaa ata aac aac cgc ccc gac tgg gtg aaa atc cca ctc gag gcg	1171
Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala	
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<210> 1156

<211> 363

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1156

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 20 25 30

Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu
 35 40 45

Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu
 50 55 60

Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile
 65 70 75 80

Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile
 85 90 95

Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser
 100 105 110

Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro
 115 120 125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala
 130 135 140

Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly
 145 150 155 160

Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala
 165 170 175

Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser
 180 185 190

Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu
 195 200 205

Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg
 210 215 220

Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala
 225 230 235 240

His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys
 245 250 255

Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg
 260 265 270

Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala
 275 280 285

Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His

290	295	300
Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly 305 310 315 320		
Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala 325 330 335		
Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys 340 345 350		
Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp 355 360		